

GenCore version 5.1.6  
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in search, using sw model

ril 2, 2004, 10:11:59 ; Search time 54 Seconds  
(without alignments)  
612.186 Million cell updates/sec

-10-066-273-9

9  
MIVFGWAVFLASRSLGQGLL.....QNVDGLVLDLAVIRTLVDK 117

OSUM62

pop 10.0 , Gapext 0.5

86107 seqs, 282547505 residues

ts satisfying chosen parameters: 1586107

gth: 0  
gth: 2000000000

inimum Match 0%  
aximum Match 100%  
isting first 45 summaries

Geneseq\_29Jan04:\*  
Geneseqp1980s:\*  
Geneseqp1990s:\*  
Geneseqp2000s:\*  
Geneseqp2001s:\*  
Geneseqp2002s:\*  
Geneseqp2003as:\*  
Geneseqp2003bs:\*  
Geneseqp2004s:\*

the number of results predicted by chance to have a  
r than or equal to the score of the result being printed,  
ed by analysis of the total score distribution.

SUMMARIES

ery	ch	Length	DB	ID	Description
0.0	117	4	AAB31180	Aab31180	Amino aci
0.0	117	6	ABO25151	Novel hum	
0.0	117	6	ABU67269	Novel hum	
0.0	117	6	ABU72037	Novel hum	
0.0	117	6	ABU67138	Novel hum	
0.0	117	6	ABU79780	Human sec	
0.0	117	6	ABO33583	Novel hum	
0.0	117	6	ADA47181	Human sec	
0.0	117	7	ABO44436	Human sec	
0.0	117	7	ABO33460	Novel hum	
0.0	117	7	ABO19838	Human sec	
0.0	117	7	ADCI7875	Human PRO	
0.0	117	7	ADD10295	Human sec	
0.0	117	7	ADD11255	Human sec	
0.0	117	7	ADD70521	Human sec	
0.0	117	7	ADD39598	Human sec	
0.0	117	7	ADD70044	Human sec	
0.0	117	7	ADD37048	Human sec	
0.0	117	7	ADD38165	Human sec	
0.0	117	7	ADD39121	Human sec	
0.0	117	7	ADD38644	Human sec	
0.0	117	7	ADD40075	Human sec	
0.0	117	7	ADE50296	Human sec	
0.0	117	7	ADE19908	Human sec	
0.0	117	7	ADE49819	Human sec	

26	609	100.0	117	7	ADE21377	Hi
27	609	100.0	117	8	ADE41256	Hi
28	609	100.0	117	8	ADE41104	Hi
29	609	100.0	118	3	AAY99341	Hi
30	609	100.0	118	4	AAB66090	Pi
31	609	100.0	118	5	ABB84819	Hi
32	609	100.0	118	5	ABB95425	Hi
33	604	99.2	289	4	AAM25871	Hi
34	604	99.2	427	2	AAY25761	Hi
35	604	99.2	427	3	AAB32412	Hi
36	604	99.2	436	3	AAB32411	Hi
37	604	99.2	576	3	AAB32384	Hi
38	604	99.2	576	4	AAB94297	Hi
39	604	99.2	576	5	ABP64699	Hi
40	85	14.0	961	6	ABU21450	Pi
41	79.5	13.1	5002	4	ABB63723	Di
42	78	12.8	1527	2	AAW81172	Hi
43	78	12.8	1531	2	AAW81173	Hi
44	77	12.6	2618	4	ABG02135	Nc
45	77	12.6	2622	4	ABG06418	Nc

ALIGNMENTS

RESULT 1  
AAB31180  
ID AAB31180 standard; protein; 117 AA.  
XX  
AC AAB31180;  
XX  
DT 20-APR-2001 (first entry)  
XX  
DE Amino acid sequence of human polypeptide PRO444.  
XX  
KW Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1 PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO43 PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO26 PRO6309; cell death; genetic disorder; transgenic animal; gene tr

Homo sapiens.

Key	Peptide	Location/Qualifiers
FT	1..16	/note= "signal peptide"
FT	Modified-site	18..24
FT	Modified-site	/note= "N-myristoylation site"
FT	Modified-site	32..38
FT	Modified-site	/note= "N-myristoylation site"
FT	Modified-site	34..40
FT	Modified-site	/note= "N-myristoylation site"
FT	Modified-site	35..41
FT	Modified-site	/note= "N-myristoylation site"
FT	Modified-site	51..57
FT	Modified-site	/note= "N-myristoylation site"

WO200077037-A2.

21-DEC-2000.

22-MAY-2000; 2000WO-US014042.

15-JUN-1999; 99US-0139695P.  
20-JUL-1999; 99US-0145070P.  
26-JUL-1999; 99US-0145698P.  
17-AUG-1999; 99US-0149396P.  
01-SEP-1999; 99WO-US020111.  
08-SEP-1999; 99WO-US020594.  
15-SEP-1999; 99WO-US021090.  
15-SEP-1999; 99WO-US021547.  
30-NOV-1999; 99WO-US028313.

PR 99WO-US028301.  
ER 99WO-US028565.  
PR 99US-0169495P.  
PR 2000WO-US000219.  
PR 2000WO-US004341.  
PR 2000WO-US004342.  
PR 2000WO-US004414.  
PR 2000WO-US005601.  
PR 2000WO-US005841.  
PR 2000WO-US007377.  
PR 2000WO-US008439.  
PR 2000WO-US013358.  
PR 2000WO-US013705.  
PR VTECH INC.  
PR Baker KP, Botstein DA, Desnoyers L, Eaton DL;  
PR Song S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
PR Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;  
PR ay MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;  
PR ang Z;  
PR 0091/06.  
PR 3965.  
PR leic acid molecule encoding a PRO polypeptide which is a  
PR a polypeptide is useful for gene therapy and identification  
PR of polypeptides.  
PR } 4; 244pp; English.  
PR sequence represents a human secreted and transmembrane  
PR The specification describes human polypeptides, designated  
PR 14, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,  
PR 161, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO7170,  
PR 13, PRO1318, PRO1600, PRO9940, PRO5333, PRO301, PRO187,  
PR 111, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003,  
PR 150, PRO2630 and PRO6309. The biological activity of cells  
PR ated with agents that bind to these polypeptides, resulting  
PR of the cells. The polynucleotides encoding these  
PR are useful in the recombinant production of the  
PR as a hybridisation probe to screen libraries to isolate  
PR sequences, or to map the gene. They may also be used for  
PR etic disorders, and to produce transgenic animals which are  
PR le development and screening of therapeutically useful  
PR polynucleotides can also be used in gene therapy e.g. to  
PR ictive gene  
PR AA;  
PR 100.0%; Score 609; DB 4; Length 117;  
PR arity 100.0%; Pred. No.2e-63;  
PR onservative 0; Mismatches 0; Indels 0; Gaps 0;  
PR 'GWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATMGNSICRDDSGLVDTLVDK 60  
PR 'GWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATMGNSICRDDSGLVDTLVDK 60  
PR ENSAVPTADTRSPQPDVPRPPRRGRGPHPRKKQNVNDGLVDTLAVIRTLVDK 117  
PR ENSAVPTADTRSPQPDVPRPPRRGRGPHPRKKQNVNDGLVDTLAVIRTLVDK 117  
PR standard; protein; 117 AA.  
PR (first entry)  
PR secreted and transmembrane protein PRO444.

KW Human; secreted and transmembrane protein; PRO; antidiabetic;  
KW ophthalmological; cytostatic; immunostimulant; gene therapy;  
KW vascular endothelial growth factor inhibitor; hypertrophy of adu  
KW protein secretion disorder; pancreas disorder; diabetes;  
KW vascular permeability; retinal neuron cell survival; retinal dis  
KW immune response; inflammation; mononuclear cell infiltration;  
KW eosinophil infiltration; apoptosis; neoplastic growth.  
XX Homo sapiens.  
OS US2003040014-A1.  
XX 27-FEB-2003.  
XX 01-FEB-2002; 2002US-00066269.  
XX 26-AUG-1997; 97US-0056974P.  
PR 17-SEP-1997; 97US-0059115P.  
PR 18-SEP-1997; 97US-0059263P.  
PR 19-SEP-1997; 97US-0059588P.  
PR 17-OCT-1997; 97US-0062285P.  
PR 24-OCT-1997; 97US-0062816P.  
PR 24-OCT-1997; 97US-0063082P.  
PR 27-OCT-1997; 97US-0063329P.  
PR 29-OCT-1997; 97US-0063733P.  
PR 21-NOV-1997; 97US-0066364P.  
PR 25-NOV-1997; 97US-0066840P.  
PR 16-DEC-1997; 97US-0069694P.  
PR 09-FEB-1998; 98US-0074086P.  
PR 09-FEB-1998; 98US-0074092P.  
PR 25-MAR-1998; 98US-0079294P.  
PR 08-APR-1998; 98US-0081049P.  
PR 14-JUL-1998; 98WO-US014552.  
PR 10-AUG-1998; 98US-0095998P.  
PR 18-AUG-1998; 98US-0097000P.  
PR 09-SEP-1998; 98US-0099601P.  
PR 10-SEP-1998; 98US-0099803P.  
PR 10-SEP-1998; 98US-0099811P.  
PR 10-SEP-1998; 98US-0099812P.  
PR 10-SEP-1998; 98WO-US018824.  
PR 14-SEP-1998; 98WO-US019093.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98US-0100858P.  
PR 17-SEP-1998; 98WO-US019437.  
PR 24-SEP-1998; 98US-0101922P.  
PR 28-OCT-1998; 98US-0106032P.  
PR 20-NOV-1998; 98US-0109304P.  
PR 20-NOV-1998; 98WO-US024855.  
PR 25-NOV-1998; 98WO-US025190.  
PR 01-DEC-1998; 98WO-US025108.  
PR 08-MAR-1999; 99WO-US005028.  
PR 23-MAR-1999; 99US-0125778P.  
PR 02-JUN-1999; 99WO-US012252.  
PR 15-JUN-1999; 99US-0139695P.  
PR 20-JUL-1999; 99US-0145070P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 17-AUG-1999; 99US-0149396P.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 02-DEC-1999; 99WO-US028565.  
PR 07-DEC-1999; 99US-0169495P.  
PR 20-DEC-1999; 99WO-US030999.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 09-MAR-2000; 2000WO-US006471.



2000WO-US004414.  
2000WO-US005601.  
2000WO-US005841.  
2000WO-US006471.  
2000WO-US007377.  
2000WO-US008439.  
2000WO-US013358.  
2000WO-US013705.  
2000WO-US014042.  
2000WO-US014941.  
2000WO-US015264.  
2000WO-US022031.  
2000WO-US023522.  
2000WO-US023328.  
2000WO-US032678.  
2001WO-US006520.  
2001WO-US017443.  
2001WO-US017800.  
2001WO-US019692.  
2001WO-US021066.  
2001WO-US021735.  
2001US-00002796.

NTECH INC.

Baker KP, Botstein DA, Desnovers L, Eaton DL;  
Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;  
Py MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;  
Yang Z;

1964/32.  
1925.

nucleic acids encoding novel secreted and transmembrane PRO  
useful for modulating biological activity of cell  
re polypeptide, and in chromosome and gene mapping.

4; 255pp; English.

1 describes an isolated, secreted and transmembrane  
(I), termed PRO polypeptide. (I) is useful for detecting  
1, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307,  
3004, PRO4356, PRO2630, PRO265, PRO941, fibroblast growth  
or (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for  
active molecule e.g. toxin, radiolabel or antibody, to a  
ing the polypeptides. The bioactive molecule causes cell  
is useful as hybridisation probes, in chromosome and gene  
eneration of antisense RNA and DNA, in the preparation of  
ide, for generating transgenic animals or knockout animals  
are useful in the development and screening of  
ly useful reagents, and for the genetic analysis of  
with genetic disorders, in gene therapy, and for chromosome  
n. (I) Or Ab is useful for the preparation of medicament for  
ditions which are responsive to the PRO polypeptide or anti-  
e.g. a tumour. (I) is useful for treating obesity, diabetes  
yper-insulinaemia, and cardiac insufficiency disorders, for  
mour growth, enhances vascular permeability and immune  
; inducing regeneration of auditory hair cells and for  
ing loss in mammals, and for treating bone and/or cartilage  
h as sports injuries and arthritis. This is the amino acid  
i novel human secreted and transmembrane polypeptide  
lignucleotide

AA;

100.0%; Score 609; DB 6; Length 117;  
larity 100.0%; Pred. No. 2e-63;  
onservative 0; Mismatches 0; Indels 0; Gaps 0;

RGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATMGNSICICRDDSCTDSDVDTQQ 60  
|||||  
RGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATMGNSICICRDDSCTDSDVDTQQ 60

QY 61 QQAENSAVPTADTRSQPRDPVRRRGRGPHEPRKKQNVDGLVLDTLAVIRTLV  
Db 61 QQAENSAVPTADTRSQPRDPVRRRGRGPHEPRKKQNVDGLVLDTLAVIRTLV

RESULT 4

ABU72037  
ID ABU72037 standard; protein; 117 AA.

XX AC ABU72037;

XX DT 11-JUN-2003 (first entry)

XX DE Novel human secreted and transmembrane protein PRO444.

XX KW Human; secreted and transmembrane polypeptide; PRO;  
KW fibroblast growth factor receptor; PRO533; PRO301; PRO187; PRO33  
KW PRO1411; PRO10096; PRO246; PRO6307; PRO6003; FGFR-3; FGFR-4; FGF  
KW FGFR-2; PRO6004; PRO4356; PRO2630; PRO265; PRO951; bioactive mol  
KW toxin; radiolabel; antibody; cell death; chromosome mapping;  
KW gene mapping; transgenic animal; knockout animal; gene therapy;  
KW tissue typing.

XX OS Homo sapiens.

XX PN US2002177165-A1.

XX PD 28-NOV-2002.

XX PF 01-FEB-2002; 2002US-00066500.

XX PR 26-AUG-1997; 97US-0056974P.

XX PR 17-SEP-1997; 97US-0059115P.

XX PR 18-SEP-1997; 97US-0059263P.

XX PR 19-SEP-1997; 97US-0059588P.

XX PR 17-OCT-1997; 97US-0062285P.

XX PR 24-OCT-1997; 97US-0062816P.

XX PR 24-OCT-1997; 97US-0063082P.

XX PR 27-OCT-1997; 97US-0063329P.

XX PR 29-OCT-1997; 97US-0063733P.

XX PR 21-NOV-1997; 97US-0066364P.

XX PR 25-NOV-1997; 97US-0066640P.

XX PR 16-DEC-1997; 97US-0069694P.

XX PR 09-FEB-1998; 98US-0074086P.

XX PR 09-FEB-1998; 98US-0074092P.

XX PR 25-MAR-1998; 98US-0079294P.

XX PR 08-APR-1998; 98US-0081049P.

XX PR 14-JUL-1998; 98WO-US014552.

XX PR 10-AUG-1998; 98US-0095998P.

XX PR 18-AUG-1998; 98US-0097000P.

XX PR 09-SEP-1998; 98US-0099601P.

XX PR 10-SEP-1998; 98US-0099803P.

XX PR 10-SEP-1998; 98US-0099811P.

XX PR 10-SEP-1998; 98US-0099812P.

XX PR 10-SEP-1998; 98WO-US018824.

XX PR 14-SEP-1998; 98WO-US019093.

XX PR 16-SEP-1998; 98WO-US019330.

XX PR 17-SEP-1998; 98US-0100858P.

XX PR 17-SEP-1998; 98WO-US019437.

XX PR 24-SEP-1998; 98US-0101922P.

XX PR 28-OCT-1998; 98US-0106032P.

XX PR 20-NOV-1998; 98US-0109304P.

XX PR 20-NOV-1998; 98WO-US024855.

XX PR 25-NOV-1998; 98WO-US025190.

XX PR 01-DEC-1998; 98WO-US025108.

XX PR 08-MAR-1999; 99WO-US005028.

XX PR 23-MAR-1999; 99US-0125778P.

XX PR 02-JUN-1999; 99WO-US012252.

XX PR 15-JUN-1999; 99US-0139695P.

XX PR 20-JUL-1999; 99US-0145070P.

XX PR 26-JUL-1999; 99US-0145698P.

XX PR 17-AUG-1999; 99US-0149396P.



99WO-US020111.  
99WO-US020594.  
99WO-US021090.  
99WO-US021547.  
99WO-US028313.  
99WO-US028301.  
99WO-US028565.  
99US-0169495P.  
99WO-US030999.  
2000WO-US000219.  
2000WO-US004341.  
2000WO-US004342.  
2000WO-US004414.  
2000WO-US005601.  
2000WO-US005841.  
2000WO-US006471.  
2000WO-US007377.  
2000WO-US008439.  
2000WO-US013358.  
2000WO-US013705.  
2000WO-US014042.  
2000WO-US014941.  
2000WO-US015264.  
2000WO-US022031.  
2000WO-US023522.  
2000WO-US023328.  
2000WO-US032678.  
2001WO-US006520.  
2001WO-US017443.  
2001WO-US017800.  
2001WO-US019692.  
2001WO-US021066.  
2001WO-US021735.  
2001US-00002796.

TECH INC.

Baker KP, Botstein DA, Desnoyers L, Eaton DL,  
ong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;  
Y MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;  
ng Z;

482/31.  
455.

d and transmembrane polypeptide for modulating biological  
ell expressing the polypeptide, for identifying agonists or  
f polypeptide, and as molecular weight markers.

4; 254pp; English.

describes an isolated, secreted and transmembrane  
PP), termed PRO PP or fibroblast growth factor receptor PP  
seful for detecting PRO533, PRO301, PRO187, PRO337, PRO1411,  
246, PRO6307, PRO6003, fibroblast growth factor receptor  
R-4, FGFR-1, FGFR-2, PRO6004, PRO4356, PRO2630, PRO265 or  
ptide, and for linking a bioactive molecule to a cell  
e above polypeptides. The bioactive molecule, a toxin,  
an antibody, causes cell death. PRO is useful in assays to  
r proteins or molecules involved in binding interaction. The  
e (II) encoding (I) is useful in chromosome and gene  
eneration of antisense RNA and DNA, for generating  
imals or knockout animals which in turn are useful in the  
nd screening of therapeutically useful reagents, to  
ridisation probes for mapping the gene which encodes the PRO  
netic analysis of individuals with genetic disorders, in  
for chromosome identification and as a chromosome marker.  
are useful for tissue typing. This is the amino acid  
novel human secreted and transmembrane PRO polypeptide

AA;

Query Match 100.0%; Score 609; DB 6; Length 117;  
Best Local Similarity 100.0%; Pred. No. 2e-63;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; (

QY 1 MIVFGWAVFLASRSLGQGLLTLEEHIAHFLGTGGAATTMGNSICRDDSGTDDSY  
Db 1 MIVFGWAVFLASRSLGQGLLTLEEHIAHFLGTGGAATTMGNSICRDDSGTDDSY  
QY 61 QQAENSAPTADTRSQPRDPVPRRRGRGPHPRRKKQNVGGLVLDLTLAVIRTLVI  
Db 61 QQAENSAPTADTRSQPRDPVPRRRGRGPHPRRKKQNVGGLVLDLTLAVIRTLVI

RESULT 5

ABU67138

ID ABU67138 standard; protein; 117 AA.

XX ABU67138;

DT 28-MAY-2003 (first entry)

DE Novel human secreted and transmembrane protein PRO444.

Secreted and transmembrane polypeptide; PRO polypeptide; PRO533;  
PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003; PRO  
PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;  
fibroblast growth factor receptor; cell death; chromosome mapping  
gene mapping; transgenic animal; knockout animal; gene therapy; t  
obesity; diabetes; insulinemia; vascular permeability;  
cardiac insufficiency disorder; immune response; hearing loss;  
auditory hair cell regeneration; bone disorder; cartilage disorde  
sports injury; arthritis.

OS Homo sapiens.

XX US2003032062-A1.

PN 13-FEB-2003.

XX 01-FEB-2002; 2002US-00066273.

PR 26-AUG-1997; 97US-0056974P.  
PR 17-SEP-1997; 97US-0059115P.  
PR 18-SEP-1997; 97US-0059263P.  
PR 19-SEP-1997; 97US-0059588P.  
PR 17-OCT-1997; 97US-0062285P.  
PR 24-OCT-1997; 97US-0062816P.  
PR 24-OCT-1997; 97US-0063082P.  
PR 27-OCT-1997; 97US-0063329P.  
PR 29-OCT-1997; 97US-0063733P.  
PR 21-NOV-1997; 97US-0066364P.  
PR 25-NOV-1997; 97US-0066840P.  
PR 16-DEC-1997; 97US-0069694P.  
PR 09-FEB-1998; 98US-0074086P.  
PR 09-FEB-1998; 98US-0074092P.  
PR 25-MAR-1998; 98US-0079294P.  
PR 08-APR-1998; 98US-0081049P.  
PR 14-JUL-1998; 98WO-US014552.  
PR 10-AUG-1998; 98US-0095998P.  
PR 18-AUG-1998; 98US-0097000P.  
PR 09-SEP-1998; 98US-0099601P.  
PR 10-SEP-1998; 98US-0099803P.  
PR 10-SEP-1998; 98US-0099811P.  
PR 10-SEP-1998; 98US-0099812P.  
PR 10-SEP-1998; 98WO-US018824.  
PR 14-SEP-1998; 98WO-US019093.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98US-0100858P.  
PR 17-SEP-1998; 98WO-US019437.  
PR 24-SEP-1998; 98US-0101922P.  
PR 28-OCT-1998; 98US-0106032P.  
PR 20-NOV-1998; 98US-0109304P.  
PR 20-NOV-1998; 98WO-US024855.

98WO-US025190.  
98WO-US025108.  
98WO-US005028.  
99US-0125778P.  
98WO-US012252.  
99US-0139695P.  
99US-0145070P.  
99US-0145698P.  
99US-0149396P.  
99WO-US020111.  
99WO-US020594.  
99WO-US021090.  
99WO-US021547.  
99WO-US028313.  
99WO-US028301.  
99WO-US028565.  
99US-0169495P.  
99WO-US030999.  
2000WO-US000219.  
2000WO-US004341.  
2000WO-US004342.  
2000WO-US004414.  
2000WO-US005601.  
2000WO-US005841.  
2000WO-US006471.  
2000WO-US007377.  
2000WO-US008439.  
2000WO-US013358.  
2000WO-US013705.  
2000WO-US014042.  
2000WO-US014941.  
2000WO-US015264.  
2000WO-US022031.  
2000WO-US023522.  
2000WO-US023328.  
2000WO-US032678.  
2001WO-US006520.  
2001WO-US017443.  
2001WO-US017800.  
2001WO-US019692.  
2001WO-US021066.  
2001WO-US021735.  
2001US-00002796.

NTECH INC.

, Baker KP, Botstein DA, Desnoyers L, Eaton DL;  
Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;  
oy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;  
ang Z;

1963/32.  
4445.

and transmembrane polypeptide for modulating biological  
a cell expressing the polypeptide, identifying agonists or  
of the polypeptide, and as molecular weight markers.

g 4; 254pp; English.

n describes an isolated, secreted and transmembrane  
(I), termed PRO polypeptide. (I) is useful for detecting  
01, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307,  
6004, PRO4356, PRO2630, PRO265, PRO941, fibroblast growth  
tor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for  
oactive molecule e.g. toxin, radiolabel or antibody, to a  
ing the polypeptides. The bioactive molecule causes cell  
Is useful as hybridisation probes, in chromosome and gene  
generation of antisense RNA and DNA, in the preparation of  
ide, for generating transgenic animals or knockout animals  
n are useful in the development and screening of  
lly useful reagents, and for the genetic analysis of

CC individuals with genetic disorders, in gene therapy, and for chr  
CC identification. (I) Or Ab is useful for the preparation of medic  
CC treating conditions which are responsive to the PRO polypeptide  
CC PRO antibody e.g. a tumour. (I) is useful for treating obesity,  
CC or hypo- or hyper-insulinaemia, and cardiac insufficiency disor  
CC inhibiting tumour growth, enhances vascular permeability and imm  
CC response, for inducing regeneration of auditory hair cells and f  
CC treating hearing loss in mammals, and for treating bone and/or c  
CC disorders such as sports injuries and arthritis. This is the ami  
CC sequence of a novel human secreted and transmembrane polypeptide  
XX  
SQ Sequence 117 AA;

Query Match 100.0%; Score 609; DB 6; Length 117;  
Best Local Similarity 100.0%; Pred. No. 2e-63;  
Matches 117; Conservative 0; Mismatches 0; Indels 0;

QY 1 MIVFGWAVFLASRSLGQLLLTLEEHIAHFLGTGGAATMGNSCICRDDSGTDD  
Db 1 MIVFGWAVFLASRSLGQLLLTLEEHIAHFLGTGGAATMGNSCICRDDSGTDD  
QY 61 QQAENSAPVTADTRSQRDPVRRPGRGPHPRRKQNVGGLVLDTLAVIRTLV  
Db 61 QQAENSAPVTADTRSQRDPVRRPGRGPHPRRKQNVGGLVLDTLAVIRTLV

RESULT 6

ABU79780  
ID ABU79780 standard; protein; 117 AA.  
XX  
AC ABU79780;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Human secreted/transmembrane protein PRO444.  
XX  
KW Human; secreted protein; transmembrane protein; PRO; genetic dis  
KW gene therapy.  
XX Homo sapiens.  
XX US2003032057-A1.  
XX  
PD 13-FEB-2003.  
XX  
PF 15-NOV-2001; 2001US-00002796.  
XX  
PR 26-AUG-1997; 97US-0056974P.  
PR 17-SEP-1997; 97US-0059115P.  
PR 18-SEP-1997; 97US-0059263P.  
PR 19-SEP-1997; 97US-0059588P.  
PR 17-OCT-1997; 97US-0062285P.  
PR 24-OCT-1997; 97US-0062816P.  
PR 24-OCT-1997; 97US-0063082P.  
PR 27-OCT-1997; 97US-0063329P.  
PR 29-OCT-1997; 97US-0063733P.  
PR 21-NOV-1997; 97US-0066364P.  
PR 25-NOV-1997; 97US-0066840P.  
PR 16-DEC-1997; 97US-0069694P.  
PR 09-FEB-1998; 98US-0074086P.  
PR 09-FEB-1998; 98US-0074092P.  
PR 25-MAR-1998; 98US-0079294P.  
PR 08-APR-1998; 98US-0081049P.  
PR 14-JUL-1998; 98WO-US014552.  
PR 10-AUG-1998; 98US-0095998P.  
PR 18-AUG-1998; 98US-0097000P.  
PR 09-SEP-1998; 98US-0099601P.  
PR 10-SEP-1998; 98US-0099803P.  
PR 10-SEP-1998; 98US-0099811P.  
PR 10-SEP-1998; 98US-0099812P.  
PR 10-SEP-1998; 98WO-US018824.  
PR 14-SEP-1998; 98WO-US019093.  
PR 16-SEP-1998; 98WO-US019330.

98US-0100858P.  
98WO-US019437.  
98US-0101922P.  
98US-0106032P.  
98US-0109304P.  
98WO-US024855.  
98WO-US025190.  
98WO-US025108.  
98WO-US005028.  
99US-0125778P.  
99WO-US012252.  
99US-0139695P.  
99US-0145070P.  
99US-0145698P.  
99US-0149396P.  
99WO-US020111.  
99WO-US020594.  
99WO-US021090.  
99WO-US021547.  
99WO-US028313.  
99WO-US028301.  
99WO-US028565.  
99US-0169495P.  
99WO-US030999.  
2000WO-US000219.  
2000WO-US004341.  
2000WO-US004342.  
2000WO-US004414.  
2000WO-US005601.  
2000WO-US005841.  
2000WO-US006471.  
2000WO-US007377.  
2000WO-US008439.  
2000WO-US013358.  
2000WO-US013705.  
2000WO-US014042.  
2000WO-US014941.  
2000WO-US015264.  
2000WO-US022031.  
2000WO-US023522.  
2000WO-US023328.  
2000WO-US032678.  
2001WO-US006520.  
2001WO-US017443.  
2001WO-US017800.  
2001WO-US019692.  
2001WO-US021066.  
2001WO-US021735.

TECH INC.

Baker KP, Botstein DA, Deenoysers L, Eaton DL,  
Gao W, Gerber H, Gerritsen ME, Goddard A,  
Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J,  
Stewart TA, Tumas D, Watanabe CK, Williams PM,  
Z;

160/32.  
186.

1 and transmembrane polypeptide for modulating biological  
all expressing the polypeptide, identifying agonists or  
polypeptide, and as molecular weight markers.

4; 255pp; English.

relates to an isolated, secreted/transmembrane polypeptide,  
ypeptide, having at least 80% sequence identity to a  
ted from any one of the 37 sequences appearing as ABU79779  
o a sequence encoded by a nucleic acid molecule deposited  
of the ATCC numbers given in the specification. Also  
in isolated nucleic acid molecule having at least 80%  
ity to a sequence selected from any one of the 37 CDNA

sequences defined in the specification (or encoding the mature PR  
protein or a PRO protein extracellular domain), a PRO expression  
a hoist cell comprising the vector, PRO fusion proteins, anti-PRC  
antibodies and a method for linking a bioactive molecule to a cel  
expressing the above PRO polypeptides, the bioactive molecule is  
radiolabel or an antibody and causes the death of the cell. PRO c  
antibody is useful for modulating at least one biological activit  
cell expressing the above polypeptides. PRO is useful for identif  
agonists or antagonists of PRO, for preparing a variant of PRO, a  
molecular weight markers for protein electrophoresis purpose and  
nucleic acid is useful for recombinantly expressing those markers  
also useful as therapeutic agent. PRO is useful in assays to iden  
other proteins or molecules involved in binding interaction. PRO  
acid is useful as hybridisation probes, in chromosome and gene ma  
in generation of antisense RNA and DNA, in the preparation of PRO  
polypeptide, in gene therapy, for generating transgenic animals o  
knockout animals which in turn are useful in the development and  
screening of therapeutically useful reagents, to construct hybrid  
probes for mapping the gene which encodes the PRO and for the gen  
analysis of individuals with genetic disorders, for chromosome  
identification, as a chromosome marker, and for generating probes  
polymerase chain reaction (PCR), Northern analysis, Southern anal  
Western analysis. The antibody is useful in diagnostic assays for  
e.g. detecting its expression in specific cells, tissues or serum  
affinity purification of PRO from recombinant cell culture or nat  
sources. PRO or Ab is useful for the preparation of medicament for  
treating conditions which is responsive to the PRO polypeptide or  
PRO antibody. PRO and PRO nucleic acid are useful for tissue typi  
present sequence encodes a PRO polypeptide

XX Sequence 117 AA;

Query Match 100.0%; Score 609; DB 6; Length 117;  
Best Local Similarity 100.0%; Pred. No. 2e-63;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; G

QY 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATMGNSICRDDS  
Db 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATMGNSICRDDS  
QY 61 QQAENSAVPTADTRSPQRPDPVPPRRGRGPHPRKKQNVNDGLVLDTLAVIRTLVD  
Db 61 QQAENSAVPTADTRSPQRPDPVPPRRGRGPHPRKKQNVNDGLVLDTLAVIRTLVD

RESULT 7

ABO33583  
ID ABO33583 standard; protein; 117 AA.  
XX  
AC ABO33583;  
XX  
DT 17-SEP-2003 (first entry)  
XX  
DE Novel human secreted and transmembrane protein PRO444.  
XX  
KW Human; secreted and transmembrane protein; PRO; angiogenesis;  
KW endothelial cell proliferation; wound healing; immune response;  
KW T-lymphocytes proliferation; neonatal heart hypertrophy; tumour;  
KW cardiac insufficiency disorder; calcium flux; inflammation;  
KW vascular endothelial growth factor-stimulated proliferation;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW nephropathy; Schanlein-Henoch purpura; celiac disease; Crohn's di  
KW dermatitis herpetiformis; diabetes; haemoglobin switch; insulinae  
KW pancreatic beta-cell precursor cell differentiation; thalassemias  
KW obesity; auditory hair cell regeneration; hearing loss; bone diso  
KW cartilage disorder; sports injury; arthritis.  
XX  
OS Homo sapiens.  
XX  
PN US2003073130-A1.  
XX  
PD 17-APR-2003.  
XX

2001US-00015869.  
PR 08-OCT-1998; 98US-0103633P.  
PR 08-OCT-1998; 98US-0103678P.  
PR 08-OCT-1998; 98US-0103679P.  
PR 08-OCT-1998; 98US-0103711P.  
PR 14-OCT-1998; 98US-0104257P.  
PR 20-OCT-1998; 98US-0104987P.  
PR 20-OCT-1998; 98US-0105000P.  
PR 20-OCT-1998; 98US-0105002P.  
PR 21-OCT-1998; 98US-0105104P.  
PR 22-OCT-1998; 98US-0105169P.  
PR 22-OCT-1998; 98US-0105266P.  
PR 26-OCT-1998; 98US-0105693P.  
PR 26-OCT-1998; 98US-0105694P.  
PR 27-OCT-1998; 98US-0105807P.  
PR 27-OCT-1998; 98US-0105881P.  
PR 27-OCT-1998; 98US-0105882P.  
PR 27-OCT-1998; 98US-0106062P.  
PR 28-OCT-1998; 98US-0106023P.  
PR 28-OCT-1998; 98US-0106029P.  
PR 28-OCT-1998; 98US-0106030P.  
PR 28-OCT-1998; 98US-0106032P.  
PR 28-OCT-1998; 98US-0106033P.  
PR 28-OCT-1998; 98US-0106178P.  
PR 29-OCT-1998; 98US-0106248P.  
PR 29-OCT-1998; 98US-0106384P.  
PR 29-OCT-1998; 98US-0108500P.  
PR 30-OCT-1998; 98US-0106464P.  
PR 03-NOV-1998; 98US-0106856P.  
PR 03-NOV-1998; 98US-0106902P.  
PR 03-NOV-1998; 98US-0106905P.  
PR 03-NOV-1998; 98US-0106919P.  
PR 03-NOV-1998; 98US-0106932P.  
PR 03-NOV-1998; 98US-0106934P.  
PR 10-NOV-1998; 98US-0107783P.  
PR 17-NOV-1998; 98US-0108775P.  
PR 17-NOV-1998; 98US-0108779P.  
PR 17-NOV-1998; 98US-0108787P.  
PR 17-NOV-1998; 98US-0108788P.  
PR 17-NOV-1998; 98US-0108801P.  
PR 17-NOV-1998; 98US-0108802P.  
PR 17-NOV-1998; 98US-0108806P.  
PR 17-NOV-1998; 98US-0108807P.  
PR 17-NOV-1998; 98US-0108867P.  
PR 17-NOV-1998; 98US-0108925P.  
PR 18-NOV-1998; 98US-0108848P.  
PR 18-NOV-1998; 98US-0108849P.  
PR 18-NOV-1998; 98US-0108850P.  
PR 18-NOV-1998; 98US-0108851P.  
PR 18-NOV-1998; 98US-0108852P.  
PR 18-NOV-1998; 98US-0108858P.  
PR 18-NOV-1998; 98US-0108904P.  
PR 22-DEC-1998; 98US-0113296P.  
PR 30-DEC-1998; 98US-0114223P.  
PR 05-JAN-1999; 99WO-US000106.  
PR 16-APR-1999; 99US-0129674P.  
PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 01-SEP-1999; 99WO-US020111.  
PR 15-SEP-1999; 99WO-US021194.  
PR 29-OCT-1999; 99US-0162506P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 02-DEC-1999; 99WO-US028551.  
PR 16-DEC-1999; 99WO-US030095.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.

PR 08-OCT-1998; 98US-0103633P.  
PR 08-OCT-1998; 98US-0103678P.  
PR 08-OCT-1998; 98US-0103679P.  
PR 08-OCT-1998; 98US-0103711P.  
PR 14-OCT-1998; 98US-0104257P.  
PR 20-OCT-1998; 98US-0104987P.  
PR 20-OCT-1998; 98US-0105000P.  
PR 20-OCT-1998; 98US-0105002P.  
PR 21-OCT-1998; 98US-0105104P.  
PR 22-OCT-1998; 98US-0105169P.  
PR 22-OCT-1998; 98US-0105266P.  
PR 26-OCT-1998; 98US-0105693P.  
PR 26-OCT-1998; 98US-0105694P.  
PR 27-OCT-1998; 98US-0105807P.  
PR 27-OCT-1998; 98US-0105881P.  
PR 27-OCT-1998; 98US-0105882P.  
PR 27-OCT-1998; 98US-0106062P.  
PR 28-OCT-1998; 98US-0106023P.  
PR 28-OCT-1998; 98US-0106029P.  
PR 28-OCT-1998; 98US-0106030P.  
PR 28-OCT-1998; 98US-0106032P.  
PR 28-OCT-1998; 98US-0106033P.  
PR 28-OCT-1998; 98US-0106178P.  
PR 29-OCT-1998; 98US-0106248P.  
PR 29-OCT-1998; 98US-0106384P.  
PR 29-OCT-1998; 98US-0108500P.  
PR 30-OCT-1998; 98US-0106464P.  
PR 03-NOV-1998; 98US-0106856P.  
PR 03-NOV-1998; 98US-0106902P.  
PR 03-NOV-1998; 98US-0106905P.  
PR 03-NOV-1998; 98US-0106919P.  
PR 03-NOV-1998; 98US-0106932P.  
PR 03-NOV-1998; 98US-0106934P.  
PR 10-NOV-1998; 98US-0107783P.  
PR 17-NOV-1998; 98US-0108775P.  
PR 17-NOV-1998; 98US-0108779P.  
PR 17-NOV-1998; 98US-0108787P.  
PR 17-NOV-1998; 98US-0108788P.  
PR 17-NOV-1998; 98US-0108801P.  
PR 17-NOV-1998; 98US-0108802P.  
PR 17-NOV-1998; 98US-0108806P.  
PR 17-NOV-1998; 98US-0108807P.  
PR 17-NOV-1998; 98US-0108867P.  
PR 17-NOV-1998; 98US-0108925P.  
PR 18-NOV-1998; 98US-0108848P.  
PR 18-NOV-1998; 98US-0108849P.  
PR 18-NOV-1998; 98US-0108850P.  
PR 18-NOV-1998; 98US-0108851P.  
PR 18-NOV-1998; 98US-0108852P.  
PR 18-NOV-1998; 98US-0108858P.  
PR 18-NOV-1998; 98US-0108904P.  
PR 22-DEC-1998; 98US-0113296P.  
PR 30-DEC-1998; 98US-0114223P.  
PR 05-JAN-1999; 99WO-US000106.  
PR 16-APR-1999; 99US-0129674P.  
PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 01-SEP-1999; 99WO-US020111.  
PR 15-SEP-1999; 99WO-US021194.  
PR 29-OCT-1999; 99US-0162506P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 02-DEC-1999; 99WO-US028551.  
PR 16-DEC-1999; 99WO-US030095.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.





ong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;  
y MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;  
ng Z;  
775/58.  
180.  
d PRO polypeptides e.g. PRO365 and PRO187, useful for  
fferentiation and/or proliferation of chondrocytes, and for  
ucose or free fatty acid uptake by skeletal muscle cells.  
3; 254pp; English.

relates to an isolated secreted/transmembrane PRO  
The polypeptide and its nucleic acid is useful as an  
vascular endothelial growth factor stimulated proliferation  
l cells, as a stimulator of T-lymphocyte proliferation, as  
endothelial cell apoptosis, c-fos and differentiation of  
ta cell precursors into mature cell, for induction of  
tion and/or proliferation of chondrocytes and for modulating  
ee fatty acid (FFA) uptake by skeletal muscle cells. The  
nd its nucleic acid is useful for generating transgenic or  
mals, for tissue typing and for chromosome identification.  
de is useful in a number of functional biological assays, as  
ght marker for protein electrophoresis, and as therapeutic  
nucleic acid is useful as a hybridisation probe, in  
d gene mapping, in the generation of antisense RNA and DNA,  
eparation PRO polypeptides. The nucleic acid is also useful  
ion probe for a cDNA library to isolate the full length PRO  
ate other cDNA and in gene therapy. The nucleic acid is also  
construction of hybridisation probes for mapping the gene  
and for the genetic analysis of individuals with the  
ders. The present sequence represents the amino acid  
human secreted/transmembrane PRO polypeptide.

AA;

100.0%; Score 609; DB 6; Length 117;  
arity 100.0%; Pred. No. 2e-63;  
onservative 0; Mismatches 0; Indels 0; Gaps 0;

GWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDSGTDSDVDTQQ 60  
|||||  
GWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDSGTDSDVDTQQ 60

NSAVPTADTRSQRDPVRPPRRGRGPHPRKKQNVGDLVLTAVIRTLVDK 117  
|||||  
NSAVPTADTRSQRDPVRPPRRGRGPHPRKKQNVGDLVLTAVIRTLVDK 117

dard; protein; 117 AA.

(first entry)

d/transmembrane protein PRO444.

ed protein; transmembrane protein; PRO; vulnery; cardiant;  
anorectic; antiarthritic; angiogenesis; cancer;  
cal capillary; endothelial cell growth; wound healing;  
lymphocyte proliferation; immune response suppression;  
t hypertrophy; cardiac insufficiency disorder;  
thelial growth factor; inflammation; mononuclear cell;  
abetes; obesity; or hyper-insulinaemia; hypo-insulinaemia;  
edifferentiation; bone disorder; cartilage disorder;  
; arthritis.

PN US2003044841-A1.  
XX 06-MAR-2003.  
XX 06-DEC-2001; 2001US-00006856.  
PF 01-SEP-1998; 98US-0098716P.  
XX 01-SEP-1998; 98US-0098723P.  
PR 01-SEP-1998; 98US-0098749P.  
PR 01-SEP-1998; 98US-0098750P.  
PR 02-SEP-1998; 98US-0098803P.  
PR 02-SEP-1998; 98US-0098821P.  
PR 02-SEP-1998; 98US-0098843P.  
PR 09-SEP-1998; 98US-0099536P.  
PR 09-SEP-1998; 98US-0099596P.  
PR 09-SEP-1998; 98US-0099598P.  
PR 09-SEP-1998; 98US-0099602P.  
PR 09-SEP-1998; 98US-0099642P.  
PR 10-SEP-1998; 98US-0099741P.  
PR 10-SEP-1998; 98US-0099754P.  
PR 10-SEP-1998; 98US-0099763P.  
PR 10-SEP-1998; 98US-0099792P.  
PR 10-SEP-1998; 98US-0099808P.  
PR 10-SEP-1998; 98US-0099812P.  
PR 10-SEP-1998; 98US-0099815P.  
PR 10-SEP-1998; 98US-0099816P.  
PR 15-SEP-1998; 98US-0100385P.  
PR 15-SEP-1998; 98US-0100388P.  
PR 15-SEP-1998; 98US-0100390P.  
PR 16-SEP-1998; 98US-0100584P.  
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PR 16-SEP-1998; 98US-0100661P.  
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PR 17-SEP-1998; 98US-0100683P.  
PR 17-SEP-1998; 98US-0100684P.  
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PR 18-SEP-1998; 98US-0101014P.  
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PR 18-SEP-1998; 98US-0101071P.  
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PR 23-SEP-1998; 98US-0101477P.  
PR 23-SEP-1998; 98US-0101479P.  
PR 24-SEP-1998; 98US-0101738P.  
PR 24-SEP-1998; 98US-0101741P.  
PR 24-SEP-1998; 98US-0101743P.  
PR 24-SEP-1998; 98US-0101915P.  
PR 24-SEP-1998; 98US-0101916P.  
PR 29-SEP-1998; 98US-0102207P.  
PR 29-SEP-1998; 98US-0102240P.  
PR 29-SEP-1998; 98US-0102307P.  
PR 29-SEP-1998; 98US-0102330P.  
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PR 30-SEP-1998; 98US-0102484P.  
PR 30-SEP-1998; 98US-0102487P.  
PR 30-SEP-1998; 98US-0102570P.  
PR 30-SEP-1998; 98US-0102571P.  
PR 01-OCT-1998; 98US-0102684P.  
PR 01-OCT-1998; 98US-0102687P.  
PR 02-OCT-1998; 98US-0102965P.  
PR 06-OCT-1998; 98US-0103258P.  
PR 06-OCT-1998; 98US-0103449P.  
PR 07-OCT-1998; 98US-0103314P.

98US-0103315P.  
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98US-0103679P.  
98US-0103711P.  
98US-0104257P.  
98US-0104987P.  
98US-0105000P.  
98US-0105002P.  
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98US-0105169P.  
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98US-0105693P.  
98US-0105694P.  
98US-0105807P.  
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98US-0106030P.  
98US-0106032P.  
98US-0106033P.  
98US-0106178P.  
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99WO-US020111.  
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2000WO-US003565.  
2000WO-US004342.

PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
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PR 20-JUN-2001; 2001WO-US019692.  
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PR 09-JUL-2001; 2001WO-US021735.  
PR 04-SEP-2001; 2001US-00946374.  
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PA (GETH ) GENENTECH INC.  
XX  
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PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hilla  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Wata  
PI Williams PM, Wood WI;  
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DR WPI; 2003-492259/46.  
DR N-PSDB; ACH04344.  
XX  
PT Novel secreted and transmembrane polypeptides and polynucleotides  
PT encoding them useful for treating various cardiac insufficiency  
PT disorders, bone and/or cartilage disorders such as sports injuries  
PT arthritis.  
  
Query Match 100.0%; Score 609; DB 7; Length 117;  
Best Local Similarity 100.0%; Pred. No. 2e-63;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; G  
  
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Db 1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAAATMGNSCICRDDSGTDDSV  
  
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Db 61 QQAENSAPTADTRSQPRDPVRRPGRGPHPRKKQNVGDLVLDTLAVIRTLVI  
  
RESULT 10  
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ID ABO33460 standard; protein; 117 AA.  
XX  
AC ABO33460;  
XX  
DT 17-SEP-2003 (first entry)  
XX  
DE Novel human secreted and transmembrane protein PRO444.  
XX  
KW Human; secreted and transmembrane protein; PRO; gene therapy; vac  
KW tissue typing; chromosome identification; vaccine.  
XX Homo sapiens.  
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PR 01-SEP-1998; 98US-0098716P.  
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2000WO-US015264.  
2000WO-US023522.



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001WO-US019692.  
001WO-US021066.  
001WO-US021735.  
ECH INC.  
stein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
d A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
Wood WI;  
92/55.  
88.  
PRO polypeptides e.g. PRO1491 and PRO1571, useful in the  
a medicament for treating a condition responsive to PRO  
nd as therapeutic agents e.g. vaccines.  
4; 561pp; English.  
describes an isolated PRO (secreted and transmembrane)  
, having at least 80% sequence identity to a sequence  
100.0%; Score 609; DB 7; Length 117;  
urity 100.0%; Pred. NO. 2e-63;  
nservative 0; Mismatches 0; Indels 0; Gaps 0;  
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lard; protein; 117 AA.  
(first entry)  
l/transmembrane protein PRO444.  
creted and transmembrane protein; gene therapy;  
gastrointestinal ulceration; skin disease; asthma;  
inocyte differentiation; psoriasis; epithelial cancer;  
carcinoma; Alzheimer's disease; Parkinson's disease;  
teral sclerosis; inflammatory disease; organ failure;  
thritis; multiple sclerosis; atherosclerosis; infertility;  
birth defect; premature aging; AIDS; cancer;  
lication; wound repair.  
al.  
2002US-00066193.  
97US-0056974P.

PR 17-SEP-1997; 97US-0059115P.  
PR 18-SEP-1997; 97US-0059263P.  
PR 19-SEP-1997; 97US-0059588P.  
PR 17-OCT-1997; 97US-0062285P.  
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PR 29-OCT-1997; 97US-0063733P.  
PR 21-NOV-1997; 97US-0066364P.  
PR 25-NOV-1997; 97US-0066840P.  
PR 16-DEC-1997; 97US-0069694P.  
PR 09-FEB-1998; 98US-0074086P.  
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PR 25-MAR-1998; 98US-0079294P.  
PR 08-APR-1998; 98US-0081049P.  
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PR 10-SEP-1998; 98US-0099803P.  
PR 10-SEP-1998; 98US-0099811P.  
PR 10-SEP-1998; 98US-0099812P.  
PR 14-SEP-1998; 98WO-US019093.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98US-0100858P.  
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PR 20-NOV-1998; 98US-0109304P.  
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PR 15-JUN-1999; 99US-0139695P.  
PR 20-JUL-1999; 99US-0145070P.  
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PR 17-AUG-1999; 99US-0149396P.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 02-DEC-1999; 99WO-US028565.  
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PR 20-DEC-1999; 99WO-US030999.  
PR 05-JAN-2000; 2000WO-US000219.  
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PR 30-MAR-2000; 2000WO-US008439.  
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PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 30-MAY-2001; 2001WO-US017443.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 15-NOV-2001; 2001US-00002796.  
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PR 15-SEP-1999; 99WO-US021194.  
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PR 30-NOV-1999; 99WO-US028313.  
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PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
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PR 15-MAR-2000; 2000WO-US006884.  
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PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 04-SEP-2001; 2001US-00946374.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hilla  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Wata  
PI Williams PM, Wood WI;  
XX  
DR WPI; 2003-555602/52.  
DR N-PSDB; ADC17874.  
XX  
PT Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful  
PT preparation of a medicament for treating a condition responsive t  
PT polypeptide, and as therapeutic agents e.g. vaccines.  
XX  
PS Claim 12; SEQ ID NO 6; 555pp; English.  
XX  
CC The invention relates to human PRO polypeptides and the polynucle  
CC encoding them. The sequences are useful in the preparation of a  
CC medicament for treating a condition responsive to a PRO polypepti  
CC polypeptides are useful in a number of functional biological assa  
CC molecular weight markers for protein electrophoresis and as thera

Query Match 100.0%; Score 609; DB 7; Length 117;  
Best Local Similarity 100.0%; Pred. NO. 2e-63;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; G

QY 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSV  
Db 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSV  
QY 61 QQAENSAPTADTRSQRPDPVPPRRGRGPHPRKKQNVGGLVLTTLAVIRTLVD  
Db 61 QQAENSAPTADTRSQRPDPVPPRRGRGPHPRKKQNVGGLVLTTLAVIRTLVD

RESULT 13  
ADD10295  
ID ADD10295 standard; protein; 117 AA.  
XX  
AC ADD10295;  
XX  
DT 01-JAN-2004 (first entry)  
XX  
DE Human secreted/transmembrane PRO polypeptide #3.

sed protein; transmembrane protein; cardiovascular disorder;  
disorder; angiogenic disorder; myocardial infarction;  
rtrophy; trauma; cancer; age-related macular degeneration;  
; endothelial cell apoptosis; smooth muscle cell growth;  
cell tube formation.  
-A1.  
2002US-00223084.  
2000US-0232887P.  
2001WO-US019692.  
2001WO-US021735.  
2002US-00081056.  
TECH INC.  
errara N, Gerber H, Gerritsen ME, Goddard A;  
Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;  
Williams PM, Wood WI, Ye W;  
0831/76.  
0294.  
nucleic acid encoding a secreted and transmembrane  
or treating a cardiovascular, endothelial, or angiogenic  
a mammal, such as cancer or age-related macular degeneration.  
ID NO 6; 493pp; English.  
l relates to an isolated nucleic acid encoding a secreted and  
polypeptide (PRO). The nucleic acid, a polypeptide encoded  
c acid, or an agonist or antagonist, is used to treat a  
r, endothelial, or angiogenic disorder in a mammal,  
ic hypertrophy, trauma, a cancer, or age-related macular  
The cardiac hypertrophy is characterised by the presence of  
level of PGF-2 alpha. A PRO polypeptide, given in the  
l, or an agonist is used to inhibit or stimulate endothelial  
n a mammal. PRO21 or an agonist is used to induce cardiac  
PRO1376 or PRO1449 is used to stimulate angiogenesis.  
agonist is used to induce endothelial cell apoptosis. A PRO  
given in the specification, or an agonist is used to  
inhibit smooth muscle cell growth, or to induce endothelial  
ation. The present sequence represents the amino acid  
PRO polypeptide of the invention.  
AA;  
arity 100.0%; Score 609; DB 7; Length 117;  
onservative 0; Mismatches 0; Indels 0; Gaps 0;  
GWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGDTSVDTQQ 60  
GWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGDTSVDTQQ 60  
NSAVPTADTRSQPRDPVPRPRRGPGPHEPRKKQNV DGLVLDTLAVIRTLVDK 117  
NSAVPTADTRSQPRDPVPRPRRGPGPHEPRKKQNV DGLVLDTLAVIRTLVDK 117  
idard; protein; 117 AA.

DT 01-JAN-2004 (first entry)  
XX Human secreted/transmembrane PRO polypeptide #3.  
DE human; secreted protein; transmembrane protein; cardiovascular d  
XX endothelial disorder; angiogenic disorder; myocardial infarction  
KW cardiac hypertrophy; trauma; cancer; age-related macular degener  
KW angiogenesis; endothelial cell apoptosis; smooth muscle cell gro  
XX endothelial cell tube formation.  
OS Homo sapiens.  
XX US2003105013-A1.  
XX 05-JUN-2003.  
PD 16-AUG-2002; 2002US-00223090.  
XX 20-JUN-2001; 2001WO-US019692.  
PF 09-JUL-2001; 2001WO-US021735.  
PR 20-FEB-2002; 2002US-00081056.  
XX (GETH ) GENENTECH INC.  
PA Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A; Step  
XX Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, W  
PI Watanabe CK, Williams PM, Wood WI, Ye W;  
XX WPI; 2003-801242/75.  
DR N-PSDB; ADD11254.  
XX New isolated nucleic acid encoding a secreted and transmembrane  
PT polypeptide, useful for treating a cardiovascular, endothelial,  
PT angiogenic disorder in a mammal, such as cancer or age-related m  
PT degeneration.  
XX Claim 11; SEQ ID NO 6; 493pp; English.  
PS The invention relates to an isolated nucleic acid encoding a sec  
XX transmembrane polypeptide (PRO). The nucleic acid, a polypeptide  
CC by the nucleic acid, or an agonist or antagonist, is used to tre  
CC cardiovascular, endothelial, or angiogenic disorder in a mammal,  
CC preferably a human. The human may have suffered a myocardial inf  
CC or has cardiac hypertrophy, trauma, a cancer, or age-related mac  
CC degeneration. The cardiac hypertrophy is characterised by the pr  
CC an elevated level of PGF-2 alpha. A PRO polypeptide, given in th  
CC specification, or an agonist is used to inhibit or stimulate end  
CC cell growth in a mammal. PRO21 or an agonist is used to induce c  
CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesi  
CC PRO4302 or an agonist is used to induce endothelial cell apoptos  
CC polypeptide, given in the specification, or an agonist is used t  
CC stimulate or inhibit smooth muscle cell growth, or to induce end  
CC cell tube formation. The present sequence represents the amino a  
CC sequence of a PRO polypeptide of the invention.  
XX Sequence 117 AA;  
SQ Query Match 100.0%; Score 609; DB 7; Length 117;  
Best Local Similarity 100.0%; Pred. No. 2e-63;  
Matches 117; Conservative 0; Mismatches 0; Indels 0;  
QY 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGDTSV  
Db 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGDTSV  
QY 61 QQAENS AVPTADTRSQPRDPVPRPRRGPGPHEPRKKQNV DGLVLDTLAVIRTLVI  
Db 61 QQAENS AVPTADTRSQPRDPVPRPRRGPGPHEPRKKQNV DGLVLDTLAVIRTLVI  
RESULT 15  
ADD70521  
ID ADD70521 standard; protein; 117 AA.





98US-0114223P.  
99WO-US000106.  
99US-0129674P.  
99US-0141037P.  
99US-0144758P.  
99US-0145698P.  
99WO-US020111.  
99WO-US021194.  
99US-0162506P.  
99WO-US028313.  
99WO-US028551.  
99WO-US030095.  
2000WO-US000219.  
2000WO-US000376.  
2000WO-US003565.  
2000WO-US004342.  
2000WO-US005004.  
2000WO-US005841.  
2000WO-US006884.  
2000WO-US013705.  
2000WO-US014042.  
2000WO-US014941.  
2000WO-US015264.  
2000WO-US023522.  
2000WO-US023328.  
2000WO-US030952.  
2000WO-US030873.  
2000WO-US032678.  
2001WO-US006520.  
2001WO-US006666.  
2001WO-US017800.  
2001WO-US019692.  
2001WO-US021066.  
2001WO-US021735.  
2001US-00946374.

TECH INC.

tstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
rd A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
Wood WI;

602/81.  
520.

3 PRO polypeptides e.g., PRO1130, PRO1275, PRO1418, PRO1555,  
t glucose or free fatty acid (FFA) uptake by skeletal muscle  
useful for treating diabetes or hyper- or hypo-insulinemia.

ID NO 6; 553pp; English.

relates to an isolated PRO polypeptide (secreted or

100.0%; Score 609; DB 7; Length 117;  
arity 100.0%; Pred. No. 2e-63;  
nservative 0; Mismatches 0; Indels 0; Gaps 0;

3WAVFLASRLGQGLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60  
|||||  
3WAVFLASRLGQGLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60

NSAVPTADTRSQRDPVPRPRGRGPHEPRRKQNVLDGLVLDTLAVIRTLVDK 117  
|||||  
NSAVPTADTRSQRDPVPRPRGRGPHEPRRKQNVLDGLVLDTLAVIRTLVDK 117

April 2, 2004, 10:24:42

GenCore version 5.1.6  
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in search, using sw model

File 2, 2004, 10:12:49 ; Search time 17 Seconds  
(without alignments)  
358.365 Million cell updates/sec

10-066-273-9

IVFGWAVFLASRLGQGLL.....QNV DGLVLTAVIRTLVDK 117

SUM62

Gap 10.0 , Gapext 0.5

681 seqs, 52070155 residues

s satisfying chosen parameters: 141681

Path: 0

Path: 20000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

MissProt\_42:\*

the number of results predicted by chance to have a  
than or equal to the score of the result being printed,  
and by analysis of the total score distribution.

SUMMARIES

ID	Length	DB	ID	Description
1.0	612	1	THIC_STRCO	Q9x9u0 streptomyce
1.9	188	1	SSB_ALCEU	P59927 alcaligenes
1.8	1483	1	BALB_HUMAN	Q9uig0 homo sapien
1.3	286	1	MSA2_PLAF1	P50496 plasmodium
1.1	2505	1	CCAA_HUMAN	Q00555 homo sapien
1.0	281	1	MSA2_PLAFH	Q99319 plasmodium
1.0	353	1	TGN1_MOUSE	Q62313 mus musculu
1.0	1456	1	CAL3_HUMAN	P02461 homo sapien
1.9	262	1	MSA2_PLAF7	Q99317 plasmodium
1.9	272	1	MSA2_PLAF6	P50498 plasmodium
1.9	274	1	MSA2_PLAF6	P50497 plasmodium
1.9	287	1	MSA2_PLAF6	P19260 plasmodium
1.9	300	1	MSA2_PLAF1	Q03644 plasmodium
1.9	300	1	MSA2_PLAF2	Q03645 plasmodium
1.9	302	1	MSA2_PLAF9	Q03994 plasmodium
1.9	347	1	MSA2_PLAF2	Q03646 plasmodium
1.9	458	1	YNE1_CAEEL	P30640 caenorhabdi
1.8	1787	1	CHD3_CAEEL	Q22516 caenorhabdi
1.7	1479	1	BALB_MOUSE	Q9z277 mus musculu
1.6	3726	1	TRX_DROME	P20659 drosophila
1.5	445	1	NRH3_MOUSE	Q9z0y9 mus musculu
1.3	1944	1	CHD3_HUMAN	Q12873 homo sapien
1.2	424	1	COT1_BOVIN	Q9ttt8 bos taurin
1.2	445	1	NRH3_RAT	Q62685 rattus norv
1.2	504	1	FTSY_SYNY3	P73930 synechocyst
1.2	702	1	EXO1_YEAST	P73975 saccharomyc
1.1	399	1	SIR3_HUMAN	Q9ntg7 homo sapien
1.1	727	1	CTCF_HUMAN	P49711 homo sapien
1.1	1298	1	ICP4_HSV11	P08392 herpes simp
1.0	393	1	CIW4_HUMAN	Q9nyg8 homo sapien
1.0	1202	1	NOS3_HUMAN	P29474 homo sapien
1.0	3828	1	TRX_DROVI	Q24742 drosophila
1.9	217	1	YKR4_EBV	P30117 epstein-bar

34	66.5	10.9	268	1	EP34_HCMVA	P16768 huma
35	66.5	10.9	276	1	MSA2_PLAF8	Q99320 plas
36	66.5	10.9	343	1	GLN2_STRVR	P19432 stre
37	66.5	10.9	423	1	COT1_HUMAN	P10589 homo
38	66.5	10.9	684	1	EP84_HCMVA	P17151 huma
39	66	10.8	228	1	EFAS_HUMAN	P52803 homo
40	66	10.8	228	1	EFAS_MOUSE	O08543 mus
41	66	10.8	324	1	HE31_STRAW	Q82e76 stre
42	66	10.8	736	1	DVL2_XENLA	P51142 xeno
43	66	10.8	1021	1	MAPA_MOUSE	Q9qyr6 mus
44	66	10.8	1380	1	CYAA_LEIDO	Q27675 leis
45	66	10.8	2716	1	OSA_DROME	Q8in94 dros

ALIGNMENTS

RESULT 1  
THIC\_STRCO  
ID THIC\_STRCO STANDARD; PRT; 612 AA.  
AC Q9X9U0;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Thiamine biosynthesis protein thic.  
GN THIC OR SCO3928 OR SCQ11.11.  
OS Streptomyces coelicolor.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2) / M145;  
RX MEDLINE=21996410; PubMed=12000953;  
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,  
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,  
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M  
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S  
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.  
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,  
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor J  
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,  
RA Hopwood D.A.;  
RT "Complete genome sequence of the model actinomycete Streptomyces  
RL coelicolor A3(2).";  
RL Nature 417:141-147(2002).  
CC -!- FUNCTION: Required for the synthesis of the hydromethylpyrimidi  
CC (HMP) moiety of thiamine (4-amino-2-methyl-5-  
CC hydroxymethylpyrimidine) (By similarity).  
CC -!- PATHWAY: Thiamine biosynthesis.  
CC -!- SIMILARITY: Belongs to the thic family.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; AL939118; CAB46966.1; --  
DR F1R; T37181; T37181.  
DR HAMAP; MF 00089; --; 1.  
DR InterPro; IPR002817; Thic.  
DR Pfam; PF01964; Thic; 1.  
DR ProDom; PD007048; Thic; 1.  
DR TIGRFAMs; TIGR00190; thic; 1.  
KW Thiamine biosynthesis; Complete proteome.  
SQ SEQUENCE 612 AA; 67371 MW; 290BF2454200CF68 CRC64;

Query Match 13.0%; Score 79; DB 1; Length 612;  
Best Local Similarity 31.2%; Pred. No. 2.4;  
Matches 30; Conservative 7; Mismatches 37; Indels 22; G







pe, alpha-1 polypeptide isoform 4) (Brain calcium channel  
(CNL1A4 OR CACH4 OR CACN3.  
(Human).  
atazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
heria; Primates; Catarrhini; Hominidae; Homo.  
06;  
1 N.A. (ISOFORMS BI-1-GGCAG/1A-1 AND BI-1/1A-2).  
1;  
614; PubMed=10049321;  
itia A., Deal C., Brust P.F., Stauderman K., Ellis S.B.,  
Johnson E.C., Williams M.E.;  
lements in domain IV that influence biophysical and  
al properties of human alpha1A-containing high-voltage-  
cium channels.";  
6:1384-1400(1999).  
1 N.A. (ISOFORM BI-1(V1)), AND VARIANTS FHM.  
llum;  
792; PubMed=8898206;  
Terwindt G.M., Vergouwe M.N., van Eijk R., Oefner P.J.,  
i., Lamerdin J.E., Mohrenweiser H.W., Bulman D.E.,  
aan J., Lindhout D., van Ommen G.-J.B., Hofker M.H.,  
Frants R.R.;  
iplegic migraine and episodic ataxia type-2 are caused by  
the Ca2+ channel gene CACNL1A4.";  
52(1996).  
1 N.A., AND ALTERNATIVE SPLICING.  
920; PubMed=8988170;  
Bailey J., Bonnen P.E., Ashizawa T., Stockton D.W.,  
ns W.B., Subramony S.H., Zoghbi H.Y., Lee C.C.;  
ninant cerebellar ataxia (SCA6) associated with small  
expansions in the alpha 1A-voltage-dependent calcium  
5:62-69(1997).  
233-1651 FROM N.A.  
McCready P.M., Skowronski E., Adamson A.W.,  
ltz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,  
isco N., Do L., Regala W., Terry A., Garnes J.,  
Poundstone P., Christensen M., Georgescu A., Avila J.,  
C., Andreise T., Trankheim M., Amico-Keller G.,  
Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,  
Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,  
Olsen A.S., Carrano A.V.;  
L-1998) to the EMBL/GenBank/DBJ databases.  
693-1807 FROM N.A.  
arcinoma;  
449; PubMed=7823133;  
Viglione M.P., Kim Y.I., Froehner S.C.;  
nd antibody inhibition of P-type calcium channels in  
ell lung carcinoma cells.";  
15:274-283(1995).  
038-2258 FROM N.A.  
l cortex;  
310; PubMed=8525433;  
Breschel T.S., Li S.H., Kidwai A.S., Antonarakis S.E.,  
Ross C.A.;  
tion of cDNA clones containing CCA trinucleotide repeats  
human brain.";  
401. Genet. 21:279-284(1995).  
Voltage-sensitive calcium channels (VSCC) mediate the  
calcium ions into excitable cells and are also involved  
ety of calcium-dependent processes, including muscle  
on, hormone or neurotransmitter release, gene expression,  
lity, cell division and cell death. The isoform alpha-1A  
se to P and/or Q-type calcium currents. P/Q-type calcium  
belong to the "high-voltage activated" (HVA) group and

are blocked by the funnel toxin (Ptx) and by the omega-agato-  
IVA (omega-Aga-IVA). They are however insensitive to  
dihydropyridines (DHP), and omega-conotoxin-GVIA (omega-CTX-  
-1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT  
COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SU  
IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE  
FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES  
SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM  
CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DE  
LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.  
-1- SUBCELLULAR LOCATION: Integral membrane protein.  
-1- ALTERNATIVE PRODUCTS:  
Event=Alternative splicing; Named isoforms=7;  
Comment=Additional isoforms seem to exist;  
Name=BI-1-GGCAG; Synonyms=1A-1;  
IsoId=000555-1; Sequence=Displayed;  
Name=BI-1; Synonyms=1A-2;  
IsoId=000555-2; Sequence=VSP\_000875;  
Name=BI-1(V1);  
IsoId=000555-3; Sequence=VSP\_000871, VSP\_000875;  
Name=BI-1(V1)-GGCAG;  
IsoId=000555-4; Sequence=VSP\_000871;  
Name=BI-1(V2);  
IsoId=000555-5; Sequence=VSP\_000872;  
Name=BI-1(V2)-GGCAG;  
IsoId=000555-6; Sequence=VSP\_000872;  
Name=BI-1(V2,V3);  
IsoId=000555-7; Sequence=VSP\_000873, VSP\_000874;  
-1- TISSUE SPECIFICITY: Brain specific; mainly found in cerebell  
cerebral cortex, thalamus and hypothalamus. No expression in  
heart, kidney, liver or muscle. Purkinje cells contain  
predominantly P-type VSCC, the Q-type being a prominent calc  
current in cerebellar granule cells.  
-1- DOMAIN: Each of the four internal repeats contains five  
hydrophobic transmembrane segments (S1, S2, S3, S5, S6) and  
positively charged transmembrane segment (S4). S4 segments  
probably represent the voltage-sensor and are characterized  
series of positively charged amino acids at every third posi  
-1- POLYMORPHISM: The poly-Gln region of CACNA1A is polymorphic:  
17 repeats in the normal population, expanded to about 21 to  
repeats in spinocerebellar ataxia 6 (SCA6) patients. There s  
to be a correlation between the repeat number and earlier on  
the disorder.  
-1- DISEASE: Defects in CACNA1A are the cause of spinocerebellar  
ataxia type 6 (SCA6) [MIM:183086]. SCA6 is an autosomal domi  
disorder characterized by slowly progressive cerebellar atax  
the limbs and gait, dysarthria, nystagmus, and mild vibratory  
proprioceptive sensory loss. These symptoms are probably exp  
by severe loss of cerebellar Purkinje cells. SCA6 is cause by  
expansion of a CAG repeat in the coding region of CACNA1A.  
-1- DISEASE: Defects in CACNA1A are the cause of familial hemipl  
migraine (FHM) [MIM:141500]; also known as migraine familial  
hemiplegic 1 (MHP1). FHM, a rare autosomal dominant subtype  
migraine with aura, is associated with ictal hemiparesis and  
some families, progressive cerebellar atrophy.  
-1- DISEASE: Defects in CACNA1A are the cause of episodic ataxia  
2 (EA-2) [MIM:108500]; also known as acetazolamide-responsiv  
hereditary paroxysmal cerebellar ataxia (APCA). This autosom  
dominant disorder is characterized by acetazolamide-responsiv  
attacks of cerebellar ataxia and migraine-like symptoms,  
interictal nystagmus, and cerebellar atrophy.  
-1- SIMILARITY: Belongs to the calcium channel alpha-1 subunits  
family.  
-----  
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-----  
EMBL; AF004884; AAB61613.1; --

1; AAB61612.1; --  
CAA68172.1; --  
-; NOT\_ANNOTATED\_CDS.  
-; NOT\_ANNOTATED\_CDS.  
AAB64179.1; --  
AAB49674.1; ALT\_INIT.  
AAB49675.1; ALT\_INIT.  
AAB49676.1; ALT\_INIT.  
AAB49677.1; ALT\_INIT.  
AAB49678.1; ALT\_INIT.  
-; AAC26839.1; --  
AAB33068.1; --  
-; NOT\_ANNOTATED\_CDS.  
188; CACNALA.  
-;  
-;  
-;  
-; P:neurogenesis; TAS.  
-; P:synaptic transmission; TAS.  
01682; Ca/Na\_pore.  
02077; Ca\_channel\_alpha.  
02111; Cat\_channel\_TrpL.  
05821; Ion\_trans.  
05820; M+channel\_nlg.  
05448; PQVDCCALPHAL.  
ion\_trans; 4.  
17; CACHANNEL.  
12; PQVDCCALPHAL.  
Transmembrane; Ion transport; Voltage-gated channel;  
1; Glycoprotein; Repeat; Multigene family;  
19; Phosphorylation; Alternative splicing; Polymorphism;  
Ion; Triplet repeat expansion.  
15 363 I.  
13 717 II.  
11 1514 III.  
11 1814 IV.  
1 98 CYTOPLASMIC (POTENTIAL).  
19 117 S1 OF REPEAT I (POTENTIAL).  
18 135 EXTRACELLULAR (POTENTIAL).  
16 155 S2 OF REPEAT I (POTENTIAL).  
16 167 CYTOPLASMIC (POTENTIAL).  
18 185 S3 OF REPEAT I (POTENTIAL).  
16 190 EXTRACELLULAR (POTENTIAL).  
1 209 S4 OF REPEAT I (POTENTIAL).  
0 228 CYTOPLASMIC (POTENTIAL).  
19 248 S5 OF REPEAT I (POTENTIAL).  
12.1%; Score 73.5; DB 1; Length 2505;  
rity 24.2%; Pred. No. 41;  
nservative 9; Mismatches 39; Indels 49; Gaps 4;  
10GLLLTLEHIAHFLGTGG-----AATMGNSC----- 44  
1EG-----REHMAHQSSSVSGSPAPSTSGTSTPRRGRQLPQTPTSTPRPHVSYS 2301  
1DSGTDSDVTQQQQAENSAV-----PTADTRSPRDPVPRRRG 87  
1AGSGPQQQQQQQQQQQAVARPGRAATSGPRRYPGTAEPLAGDRPPTGGHSSG 2361  
1PRR 95  
1ERR 2369  
STANDARD; PRT; 281 AA.  
rel. 34, Created)  
rel. 34, Last sequence update)  
rel. 34, Last annotation update)  
face antigen 2 precursor (MSA-2) (Allelic form 3).

MSA2.  
GN Plasmodium falciparum (isolate thtn / Thailand).  
OS Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OC NCBI\_TaxID=70151;  
OX [1]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=91218803; PubMed=2090943;  
RX Thomas A.W., Carr D.A., Carter J.M., Lyon J.A.;  
RA "Sequence comparison of allelic forms of the Plasmodium falciparu  
RT merozoite surface antigen MSA2.";  
RL Mol. Biochem. Parasitol. 43:211-220(1990).  
CC -!- FUNCTION: May play a role in the merozoite attachment to the  
CC erythrocyte.  
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-ancho  
CC (Potential).  
CC -!- DEVELOPMENTAL STAGE: During the trophozoite and schizont stag  
CC -----  
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CC or send an email to license@isb-sib.ch).  
CC -----  
CC EMBL; M60189; AAA29689.1; --.  
DR InterPro; IPR001136; MSA\_2.  
DR Pfam; PF00985; MSA\_2; 1.  
KW Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;  
KW GPI-anchor; Merozoite.  
FT SIGNAL 1 20 POTENTIAL.  
FT CHAIN 21 257 MEROZOITE SURFACE ANTIGEN 2.  
FT PROPEP 258 281 HYDROPHOBIC, REMOVED DURING MATURATI  
FT (BY SIMILARITY).  
FT DOMAIN 44 207 POLYMORPHIC REGION.  
FT DOMAIN 111 118 POLY-THR.  
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 254 254 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 281 AA; 28892 MW; 50598AA42D64CCBC CRC64;  
Query Match 12.0%; Score 73; DB 1; Length 281;  
Best local Similarity 35.8%; Pred. No. 4;  
Matches 24; Conservative 6; Mismatches 25; Indels 12; G.  
QY 36 AATTMGNSCICRDDSGTDDSV-----DT-----QQQAENSAVPTADTRSPRDP  
Db 152 ANTETQNNNSNVQDSQTKSNVPPTQDADTKSPTAQPEQAENSA-PTAEQTESPELQ  
QY 85 RRGGRGP 91  
Db 211 NKGTDQH 217  
RESULT 7  
TGN1\_MOUSE  
ID TGN1\_MOUSE STANDARD; PRT; 353 AA.  
AC Q62313;  
DT 15-MAR-2004 (Rel. 43, Created)  
DT 15-MAR-2004 (Rel. 43, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Trans-golgi network integral membrane protein 1 precursor (TGN38A)  
GN TGNL1 OR TGN1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ICR; TISSUE=Brain;



.533; PubMed=7540170;  
Tabashi S., Murakami K., Nakayama K.;  
Presence of two TGN38 isoforms and absence of TGN41

1. 270:14471-14476(1995).

1 N.A.  
'6J; TISSUE=Aorta, and Testis;  
'683; PubMed=12466851;  
Bruno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
Iru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
Iragi T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
Gariboldi M., Gissi C., Godzik A., Gough J.,  
Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
Waji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
Maltais L., Marchionni L., McKenzie L., Miki H.,  
Numata K., Okido T., Pavan W.J., Perteu G., Pesole G.,  
Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
Schneider C., Semple C.A., Setou M., Shimada K.,  
Sakenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
Zhan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
Iikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
Yaki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
Iizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
Yoshino M., Waterston R., Lander E.S., Rogers J.,  
Yashizaki Y.;  
The mouse transcriptome based on functional annotation of  
length cDNAs";  
3-573(2002).

1 N.A.  
1257; PubMed=12477932;  
L., Feingold E.A., Grouse L.H., Derge J.G.,  
Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,  
Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
Quellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Anton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
V., Touchman J.W., Green E.D., Dickson M.C.,  
J., Grimwood J., Schmutz J., Myers R.M.,  
S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
Schein J.E., Jones S.J.M., Marra M.A.;  
and initial analysis of more than 15,000 full-length human  
sequences";  
Acad. Sci. U.S.A. 99:16899-16903(2002).  
May be involved in regulating membrane traffic to and  
as-Golgi network.  
LAR LOCATION: Type I membrane protein. Primarily in trans-  
work. Cycles between the trans-Golgi network and the cell  
returning via endosomes (By similarity).  
SPECIFICITY: Widely expressed.  
NEOUS: Also found in strains BALB/c, C57BL/6 and DBA/2.

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CC -----  
DR EMBL; D50031; BAA08757.1; -.  
DR EMBL; AK041302; BAC30896.1; -.  
DR EMBL; AK076586; BAC36404.1; -.  
DR EMBL; BC009143; AAH09143.1; -.  
DR PIR; B56940; B56940.  
DR MGD; MGI:105080; Tgoln1.  
KW Signal; Transmembrane; Glycoprotein; Repeat; Golgi stack.  
FT SIGNAL 1 17 POTENTIAL.  
FT CHAIN 18 353 TRANS-GOLGI NETWORK INTEGRAL MEMBRAN  
FT FT PROTEIN 1.  
FT FT EXTRACELLULAR (POTENTIAL).  
FT FT TRANSMEM 299 319 POTENTIAL.  
FT FT DOMAIN 320 353 CYTOPLASMIC (POTENTIAL).  
FT FT SITE 346 349 ENDOCYTOSIS SIGNAL (BY SIMILARITY).  
FT FT DOMAIN 131 178 6 X 8 AA TANDEM REPEATS.  
FT FT REPEAT 131 138 1.  
FT FT REPEAT 139 146 2.  
FT FT REPEAT 147 154 3.  
FT FT REPEAT 155 162 4.  
FT FT REPEAT 163 170 5.  
FT FT REPEAT 171 178 6.  
FT FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 353 AA; 37848 MW; 95C340C2F4A21EB3 CRC64;  
Query Match 12.0%; Score 73; DB 1; Length 353;  
Best Local Similarity 30.5%; Pred. No. 5.1;  
Matches 18; Conservative 9; Mismatches 28; Indels 4;  
QY 32 GTGGAATTMGNSCICRDDSDVDTQQQAENSAVPTADTRSQRPDPVRRP  
Db 148 GDSGKPTAGSNKATEDDSGKSTKVLDLDPKTSKIS---PDTETSKTDKVPTEK  
RESULT 8  
CA13\_HUMAN STANDARD; PRT; 1466 AA.  
ID CA13\_HUMAN  
AC P02461; Q15112;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Collagen alpha 1(III) chain precursor.  
GN COL3A1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skin fibroblast;  
RX MEDLINE=89350838; PubMed=2764886;  
RA Ala-Kokko L., Kontusaari S., Baldwin C.T., Kuivaniemi H.,  
Prockop D.J.;  
RT "Structure of cDNA clones coding for the entire prepro alpha 1 (I  
chain of human type III procollagen. Differences in protein struc  
from type I procollagen and conservation of codon preferences.";  
RL Biochem. J. 260:509-516(1989).  
RN [2]  
RP SEQUENCE OF 149-1225 FROM N.A.  
RX MEDLINE=89386015; PubMed=2780304;  
RA Janeczko R.A., Ramirez F.;  
RT "Nucleotide and amino acid sequences of the entire human alpha 1  
(III) collagen.";  
RL Nucleic Acids Res. 17:6742-6742(1989).  
RN [3]  
RP SEQUENCE OF 168-398.  
RX MEDLINE=77134724; PubMed=557335;  
RA Seyer J.M., Kang A.H.;  
RT "Covalent structure of collagen: amino acid sequence of cyanogen





IV ASP-1050.  
7070; PubMed=2808425;  
ivaniemi H., Stolle C.A., Pope F.M., Prockop D.J.;  
mutation in the type III procollagen gene that converts  
r glycine 883 to aspartate in a mild variant of  
s syndrome IV.";  
n. 264:19313-19317(1989).

IV VAL-1077.  
4480; PubMed=1895316;  
., Lloyd J.C., Ward P.N. de Paape A., Narcisi P.,

ation of a glycine to valine substitution at amino acid  
of the triple helical region of type III collagen in a  
Ehlers-Danlos syndrome type IV.";  
-- 28:458-463(1991).

IV GLU-1173.  
2543; PubMed=1357232;  
, Richards A.J., Pope F.M., Hopkinson D.A.;

12.0%; Score 73; DB 1; Length 1466;  
 larity 28.8%; Pred. No. 25;  
 onservative 10; Mismatches 36; Indels 28; Gaps 7;

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JLLEH---IAHFLGTGAATMGNS-----CICRDDSGT--DDS 55
||| : | : ||| : ||| : 
JLLALHTIILAQOEAVEGGCSHLGQSADRDRVWKEPCQCVC--DGSVLCDDE 65
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TQQQAENS AVP --- TADTRS QRPDPVRPPRRGRGPHEPR 94  
::: | : | | | | | | | | | | | | | | |  
QELDCPNPEIPFGECCAVCPQPPTATPRPP-NGGPGQGPK 108

STANDARD; PRT; 262 AA.

(Rel. 34, Created)  
(Rel. 34, Last sequence update)  
(Rel. 34, Last annotation update)  
-face antigen 2 precursor (MSA-2) (Allelic form 1)

ulciparum (isolate Camp / Malaysia),  
veolata; Apicomplexa; Haemosporida; Plasmodium.  
135;

1 N.A.  
1803; PubMed=2090943;  
Carr D.A., Carter J.M., Lyon J.A.;  
parison of allelic forms of the Plasmodium falciparum  
face antigen MSA2.";   
Parasitol. 43:211-220(1990).

May play a role in the merozoite attachment to the

**UAR LOCATION:** Attached to the membrane by a GPI-anchor

ENTAL STAGE: During the trophozoite and schizont stages.

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: AAA29687.1; -.  
001136; MSA\_2.  
; MSA\_2; 1.  
brane; Glycoprotein; Antigen; Signal; Repeat;  
erozoite.

FT	SIGNAL	1	20	POTENTIAL.
FT	CHAIN	21	238	MEROZOITE SURFACE ANTIGEN 2.
FT	PROPEP	239	262	HYDROPHOBIC, REMOVED DURING MATURAT (BY SIMILARITY).
FT				POLYMORPHIC REGION.
FT	DOMAIN	44	188	POLY-THR.
FT	DOMAIN	91	98	N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT	CARBOHYD	22	22	N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT	CARBOHYD	36	36	N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT	CARBOHYD	139	139	N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT	CARBOHYD	211	211	N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT	CARBOHYD	235	235	N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT	CARBOHYD	236	236	N-LINKED (GLCNAC. . .) (POTENTIAL) .
SQ	SEQUENCE	262 AA;	27374 MW;	72E0B2A315E9D154 CRC64;

Query Match 11.9%; Score 72.5; DB 1; Length 262;  
Best Local Similarity 37.5%; Pred. No. 4.1;  
Matches 24; Conservative 6; Mismatches 21; Indels 13;

2000 Local Similarity 37.5%,  
 Matches 24; Conservative 6; Mismatches 21; Indels 13;

Qy 39 TMGNSICRDDSGTDSV-----DT----QQQQAENSAPVTADTRSQRPDPVR  
| | | : | | : | | : | | | | | :  
Db 137 TONNSNV-QQDSOTKSNVPQTADTKSPTAOPEQAENSA-PTAEOTESPELOSA

Qy 88 RGP 91  
Db 195 TGOH -98

## RESULT 10

MSA2 PLAF7	MSA2 PLAF7	STANDARD;	PRT;	272 AA.
ID				

DT	01-OCT-1996 (Rel. 34, Created)
DT	01-OCT-1996 (Rel. 34, Last sequence update)

DT	01-OCT-1996	(Rel. 34,	Last annotation update)
DT	01-OCT-1996	(Rel. 34,	Last sequence update)

DE Merozoite surface antigen 2 precursor (MSA-2) (45 kDa merozoite  
DE surface antigen).

OS Plasmodium falciparum (isolate 3D7).

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 CS Plasmodium varicarpium (isolate SD7).

OX NCBI\_TaxID=36329;

RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=90205972; PubMed=2181307;

RA Smythe J.A., Peterson M.G., Coppel R.L., Saul A.J., Kemp D.J.,  
RA Anders R.F.;

RT "Structural diversity in the 45-kilodalton merozoite surface ant  
RT of *Plasmodium falciparum*."; RT

RL Mol. Biochem. Parasitol. 39:227-234 (1990).

```

CC      -l:- FUNCTION: May play a role in the merozoite attachment to the
CC      erythrocyte.
CC      -l:- FUNCTION: May play a role in the merozoite attachment to the

```

```

CC      erythrocyte.
CC      SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anch
CC      -|-
CC      SUBCELLULAR LOCATION: (Potential).

```

CC (Folencial).  
CC  
CC  
CC

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CC  
DB  
DR EMBL; M28891; AAA29686.1; -.  
DQ InterPro: IPR001126. MSC 2  
DP

DR InterPro; IPR001136; MSA\_2.  
DR Pfam; PF00985; MSA\_2; 1.  
DR

KW Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;  
GPI-anchor; Merozoite.

FT	SIGNAL	1	20	POTENTIAL.
FT	CHAIN	21	248	MEROZOITE SURFACE ANTIGEN 2.

FT	PROPEP	249	272	HYDROPHOBIC, REMOVED DURING MATURATION (BY SIMILARITY).
FT				

FT	DOMAIN	44	198	POLYMORPHIC REGION.
FT	DOMAIN	95	108	POLY-THR.











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in search, using sw model

ril 2, 2004, 10:21:14 ; Search time 39 Seconds  
(without alignments)  
946.555 Million cell updates/sec

-10-066-273-9  
9  
MIVFGWAVFLASRLGQGLL.....QNVDGLVLDLAVIRTLVDK 117

OSUM62

pop 10.0 , Gapext 0.5

17041 seqs, 315518202 residues

ts satisfying chosen parameters: 1017041

gth: 0  
gth: 2000000000

inimum Match 0%  
aximum Match 100%  
isting first 45 summaries

PTREMBL 25: \*  
sp\_archaea: \*  
sp\_bacteria: \*  
sp\_fungi: \*  
sp\_human: \*  
sp\_invertebrate: \*  
sp\_mammal: \*  
sp\_mhc: \*  
sp\_organelle: \*  
sp\_phase: \*  
: sp\_plant: \*  
: sp\_rodent: \*  
: sp\_virus: \*  
: sp\_vertebrate: \*  
: sp\_unclassified: \*  
: sp\_rivir: \*  
: sp\_bacteriap: \*  
: sp\_archaeap: \*

the number of results predicted by chance to have a  
than or equal to the score of the result being printed,  
ed by analysis of the total score distribution.

SUMMARIES

ary	Length	DB	ID	Description
3.2	576	4	Q96DX4	Q96dx4 homo sapien
3.2	576	6	Q95LP3	Q95lp3 macaca fasc
3.1	117	11	Q8BLS8	Q8bls8 mus musculu
1.3	576	11	Q8C039	Q8c039 mus musculu
1.3	576	11	Q8BVR6	Q8bvr6 mus musculu
4.1	601	16	Q82FI7	Q82fi7 streptomyc
4.0	290	5	Q20394	Q20394 caenorhabdi
3.1	356	10	Q9ATR4	Q9atr4 oryza sativ
3.1	388	10	Q941M8	Q94lm8 oryza sativ
3.1	388	10	Q8LN68	Q8ln68 oryza sativ
3.1	388	10	Q7Y1X7	Q7ylx7 oryza sativ
3.1	5146	5	Q9VXR3	Q9vxr3 drosophila
3.0	970	10	Q9AYF2	Q9ayf2 oryza sativ
2.9	970	10	Q7XF23	Q7xf23 oryza sativ
2.9	188	2	Q7WX07	Q7wx07 alcaligenes
2.8	179	5	Q9XZ40	Q9xz40 plasmodium

17	78	12.8	191	5	Q9U0C1	Q9u0c1 pla
18	78	12.8	203	5	Q9U0C0	Q9u0c0 pla
19	78	12.8	480	5	Q27033	Q27033 the
20	77.5	12.7	550	12	O40912	O40912 ka
21	77.5	12.7	550	12	P88903	P88903 ka
22	76.5	12.6	634	4	Q8IXW0	Q8ixw0 hom
23	76	12.5	1063	16	Q8XXH5	Q8xxh5 ra
24	75.5	12.4	948	5	Q9U304	Q9u304 cae
25	75	12.3	147	5	O15805	O15805 pla
26	75	12.3	183	5	Q9U0B5	Q9u0b5 pla
27	75	12.3	183	5	Q9U0B6	Q9u0b6 pla
28	75	12.3	204	5	Q9U0B4	Q9u0b4 pla
29	75	12.3	260	5	Q8IT83	Q8it83 pla
30	75	12.3	267	13	Q9PUV0	Q9puv0 ba
31	75	12.3	278	5	Q25862	Q25862 pla
32	75	12.3	291	5	Q25789	Q25789 pla
33	74.5	12.2	121	12	Q8QRK4	Q8qrk4 hei
34	74.5	12.2	462	3	O42721	O42721 peni
35	74.5	12.2	2120	5	Q8IAK1	Q8iak1 pla
36	74	12.2	850	16	Q8FML9	Q8fml9 cor
37	73.5	12.1	416	12	Q81265	Q81265 hei
38	73	12.0	206	5	Q9U0C3	Q9u0c3 pla
39	73	12.0	220	5	Q9U0B3	Q9u0b3 pla
40	73	12.0	222	5	Q9U0B1	Q9u0b1 pla
41	73	12.0	353	11	Q62313	Q62313 mus
42	73	12.0	579	2	Q8GFF2	Q8gff2 stre
43	73	12.0	1160	5	Q8T0V9	Q8t0v9 droe
44	73	12.0	1163	4	Q8N6U4	Q8n6u4 hom
45	73	12.0	3571	10	Q9SL27	Q9sl27 ara

ALIGNMENTS

RESULT 1  
Q96DX4  
ID Q96DX4 PRELIMINARY; PRT; 576 AA.  
AC Q96DX4;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Hypothetical protein KIAA1972.  
GN KIAA1972.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymph;  
RA Strausberg R.;  
RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=21842142; PubMed=11853319;  
RA Nagase T., Kikuno R., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes.  
RT The complete sequences of 50 new cDNA clones which code for large  
RT proteins.";  
RL DNA Res. 8:319-327(2001).  
DR EMBL; BC013173; AAH13173.1; -.  
DR EMBL; AB075852; BAB85558.1; -.  
DR InterPro; IPR008938; ARM.  
DR InterPro; IPR003877; SPRY receptor.  
DR Pfam; PF00622; SPRY; 1.  
DR SMART; SM00184; RING; 1.  
DR SMART; SM00449; SPRY; 1.  
DR PROSITE; PS50089; ZF\_RING\_2; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 576 AA; 64180 MW; 8598E43E96691F9B CRC64;

99.2%; Score 604; DB 4; Length 576;  
arity 100.0%; Pred. No. 1.2e-57;  
onservative 0; Mismatches 0; Indels 0; Gaps 0;  
GWAFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60  
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GWAFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60  
NSAVPTADTRSQRDPVPRPPRRGRGPHEPRRKQNVGDLVLTAVIRTLVD 116  
|||||  
NSAVPTADTRSQRDPVPRPPRRGRGPHEPRRKQNVGDLVLTAVIRTLVD 116  
RELIMINARY; PRT; 576 AA.  
TREMBlrel. 19, Created)  
TREMBlrel. 19, Last sequence update)  
TREMBlrel. 25, Last annotation update)  
protein.  
ularis (Crab eating macaque) (Cynomolgus monkey).  
tazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
heria; Primates; Catarrhini; Cercopithecidae;  
ae; Macaca.  
41;  
N.A.  
; Osada N., Hida M., Kusuda J., Tanuma R., Hirai M.,  
ano S.;  
novel full-length cDNA clones from macaque testis cDNA  
T-2001) to the EMBL/GenBank/DBJ databases.  
5; BAB69714.1; -.  
008938; ARM.  
003877; SPRY receptor.  
001841; Znf\_ring.  
; SPRY; 1.  
4; RING; 1.  
9; SPRY; 1.  
089; ZF\_RING\_2; 1.  
protein.  
6 AA; 64259 MW; 68D230AD1C4F5F8D CRC64;  
arity 96.2%; Score 586; DB 6; Length 576;  
onservative 0; Mismatches 3; Indels 0; Gaps 0;  
GWAFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60  
|||||  
GWAFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQ 60  
NSAVPTADTRSQRDPVPRPPRRGRGPHEPRRKQNVGDLVLTAVIRTLVD 116  
|||||  
NSAVPTADTRSQRDPVPRPPRRGRGPHEPRRKQNVGDLVLTAVIRTLVD 116  
RELIMINARY; PRT; 117 AA.  
TREMBlrel. 23, Created)  
TREMBlrel. 23, Last sequence update)  
TREMBlrel. 23, Last annotation update)  
SPla and the Ryanodine receptor.  
(Mouse).  
tazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
heria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
090;  
N.A.  
6J; TISSUE=Cortex;

RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotat;  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
DR EMBL; AK043522; BAC31566.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 117 AA; 12738 MW; D3FEC471ABD55D3C CRC64;  
Query Match 92.1%; Score 561; DB 11; Length 117;  
Best Local Similarity 91.5%; Pred. No. 9.5e-54;  
Matches 107; Conservative 3; Mismatches 7; Indels 0; C  
QY 1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSV  
Db 1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHLLGTTGATATMGNSCICRDDSGAEDN  
QY 61 QQAENSAVPTADTRSQRDPVPRPPRRGRGPHEPRRKQNVGDLVLTAVIRTLV  
Db 61 QQAENSTVPTADRSRSPQPRDPVPRPPRRGRGPHEPRRKQNVGDLVLTAVIRTLV  
RESULT 4  
Q8C039 PRELIMINARY; PRT; 576 AA.  
AC Q8C039;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Hypothetical SPla and the Ryanodine receptor.  
GN 4930470D19RIK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotat;  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
DR EMBL; AK032416; BAC27858.1; -.  
DR MGD; MGI:1914860; 4930470D19RIK.  
DR InterPro; IPR008938; ARM.  
DR InterPro; IPR003877; SPRY receptor.  
DR InterPro; IPR001841; Znf\_ring.  
DR Pfam; PF00622; SPRY; 1.  
DR SMART; SM00184; RING; 1.  
DR SMART; SM00449; SPRY; 1.  
DR PROSITE; PS00089; ZF\_RING\_2; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 576 AA; 64340 MW; D72D60E803911D02 CRC64;  
Query Match 91.3%; Score 556; DB 11; Length 576;  
Best Local Similarity 91.4%; Pred. No. 2.2e-52;  
Matches 106; Conservative 3; Mismatches 7; Indels 0; C  
QY 1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSV  
Db 1 MIVFGWAVFLASRSLGQGLLLTLEEHIAHLLGTTGATATMGNSCICRDDSGAEDN  
QY 61 QQAENSAVPTADTRSQRDPVPRPPRRGRGPHEPRRKQNVGDLVLTAVIRTLV  
Db 61 QQAENSTVPTADRSRSPQPRDPVPRPPRRGRGPHEPRRKQNVGDLVLTAVIRTLV  
RESULT 5  
Q8BVR6 PRELIMINARY; PRT; 576 AA.  
ID Q8BVR6





!C-1995) to the EMBL/GenBank/DBJ databases.

[ N.A.  
1613; PubMed=9851916;

ence of the nematode *C.elegans*: A platform for  
; biology." ;  
; 012-2018(1998).  
CAA92602.1; -.  
T22161.

012.6; CE03330.  
00 AA: 32831 MW; B60BEFE9C89E7780 CRC64;

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14.0%; Score 85.5; DB 5; Length 290;
arity 30.0%; Pred. No. 0.42;
conservative 15; Mismatches 31; Indels 17; Gaps 5;

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AHFLGTGGAATTMGN-SCI CRDDSGTD-----DSVDTQQQQAENSAVPTADTRSQP 77
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
7-HWRETGLAFIIRSDACRSKDDGGCDDTIDSONSKEDQERSKNSEMPLSD-----208

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TRP R R G R G P H E P R R K K Q N V D G L V L D T 107
| | : | | | | | | | | | | | | | | | |
IRK P O - - - - - E T P R R S K O R T P G P M M P T 232

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RELIMINARY; PRT; 356 AA.

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(TREMBLrel. 17, Created)
(TREMBLrel. 17, Last sequence update)
(TREMBLrel. 22, Last annotation update)
ched1 protein (Fragment).
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(Rice).  
 .ridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 u; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 ; Oryzaceae; Oryza.  
 330;

1 N.A.  
336: PubMed=11264415:

Johnson, J. A. 1990. The evolution of the teosinte branched gene among maize and wild relatives. *Genetics* 115: 1021-1034.

405333: TCP

1; TCP; 1.

1, 1

356 356

56 AA; 37

11

larity 3

Conservati

**SECRET**

CRDSTDS  
1.1.1

LEEDGSSLS

3  
4  
5  
6  
7  
8  
9  
10  
11  
12

35

347

T42

**SECRET**

# PRELIMINARY

(TREMBL)rel

11

```
13.1%; Score 79.5; DB 10; Length 388;
urity 32.3%; Pred. No. 2.7;
nservative 6; Mismatches 27; Indels 9; Gaps 1;

DDSGTDSVDTQQQAENSA-----VPTADTRSQRDPVVRPRRGRGPHEP 93
: : : : : : : : : : : : : : : : : : : : : : : : :
EDGSSSLSDGKQQQHSNPADRGGGAGDHKGAAHGHS DGKKPAKPRRAAANPKPP 238

;
;0

RELIMINARY; PRT; 388 AA.

EMBLrel. 25, Created)
EMBLrel. 25, Last sequence update)
EMBLrel. 25, Last annotation update)
hing 1.

(indica cultivar-group).
idiplantae; Streptophyta; Embryophyta; Tracheophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae;
Oryzaeae; Oryza.
46;
N.A.
36;
, Zhao Z., Zhao Y., Sun C.R., Luo D.;
il and expression analysis of OsTb1 in rice.";
-2003) to the EMBL/GenBank/DBJ databases.
; AAP37176.1; -.
; AA; 41504 MW; 8CF363D2EAA02743 CRC64;

13.1%; Score 79.5; DB 10; Length 388;
urity 32.3%; Pred. No. 2.7;
nservative 6; Mismatches 27; Indels 9; Gaps 1;

DDSGTDSVDTQQQAENSA-----VPTADTRSQRDPVVRPRRGRGPHEP 93
: : : : : : : : : : : : : : : : : : : : : : : : :
EDGSSSLSDGKQQQHSNPADRGGGAGDHKGAAHGHS DGKKPAKPRRAAANPKPP 238

;
;10

RELIMINARY; PRT; 5146 AA.

EMBLrel. 13, Created)
EMBLrel. 22, Last sequence update)
EMBLrel. 25, Last annotation update)
1.
anogaster (Fruit fly).
azoa; Arthropoda; Hexapoda; Insecta; Pterygota;
pterygota; Diptera; Brachycera; Muscomorpha;
rosophilidae; Drosophila.
27;
N.A.
ay;
06; PubMed=10731132;
alniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
3., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
ortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Rogers J.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
le C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
```

```
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M
RA Beeson K.Y., Benos P.V., Berman D.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischman
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhao Q., Zheng
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhu X., Smith
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhou S., Yao Q.A.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.
RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Scheeler F.
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.
RA Stapleton M., Strong R., Svirskaas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell
RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003500; AAF48495.2; -.
DR FlyBase; FBgn0030674; CG8184.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
```

DR GO: 0006310; P:DNA recombination; IEA.  
DR GO: 0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro: IPR000209; Peptidase\_S8.  
DR InterPro: IPR001584; Rve.  
DR Pfam: PF00665; rve; 1.  
DR PROSITE; PS00136; SUBTILASE\_ASP; 1.  
SQ SEQUENCE 970 AA; 108499 MW; 14D8F3EB056B194A CRC64;

Query Match	13.0%;	Score 79;	DB 10;	Length 970;
Best Local Similarity	27.4%;	Pred. NO. 8.8;		
Matches 31;	Conservative	12;	Mismatches 42;	Indels 28;

Qy	4	FCWAVFLASRLG---QGULLTLEEHAHFLGT-----GGAAATTM--GNSCJ
Db	551	YSWVEFMATKDEAFQHFRGFUFLRD---LEFPGSLKRIRSDNGGTLQSVOGEDSCJ

QY 50 SGTDDSVDTQQQQAENSAVPTADTRSQPRDPVRRPPRRGRGPHPRKKQNVG 10

Dd 608 SDPDDKVGSGAGOTGROAGTAST-----PP--GRPPODERSNRPDSSG 64

RESULT 14  
Q7XF23  
ID Q7XF23  
PRELIMINARY: PRT: 970 AA.

DT	01-OCT-2003	(TrEMBLrel. 25, Created)
DT	01-OCT-2003	(TrEMBLrel. 25, Last sequence update)
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)

OC Oryza sativa (Japanese rice group);  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC *Ormatocystaceae*; *Ormatocystaceae*; *Ormatocystaceae*  
 OC *Ormatocystaceae*; *Ormatocystaceae*; *Ormatocystaceae*  
 OX *Ormatocystaceae*; *Ormatocystaceae*; *Ormatocystaceae*  
 RN NCBI\_TaxID=39947;  
 RP [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Nipponbare;  
 RA The Rice Chromosome 10 Sequencing Consortium;

RT in-depth view of structure, activity, and evolution of rice  
 chromosome 10." ;  
 RL Science 300:1566-1569 (2003).  
 RN [2]  
 RP SEQUENCE FROM N.A.

RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;  
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE017089; AAP53536.1; -.  
 KW Polyprotein.  
 SQ SEQUENCE 970 AA; 108499 MW; 14D8F3EB056B194A CRC64;

QY 4 FGWAVELASRLG---QGILLTLEEHIAHFLGT-----GGAATTM--GNSCJ

QY 50 SGTDSVDTQQQQAENS AVPTADTRS QPDPVRPPRRGRGPHEPRKKQNV DG 10

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RESULT 15
Q7WX07
ID Q7WX07 PRELIMINARY; PRT; 188 AA.
AC Q7WX07;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative single-strand binding protein.

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14:34:40 2004

us-10-066-273-9.rsp

[illegible]

trophus (Ralstonia eutropha).  
lasmid pHG1.  
eobacteria; Betaproteobacteria; Burkholderiales;  
ae; Ralstonia.  
);

N.A.

Henne A., Cramm R., Eitinger T., Friedrich B.,

leotide Sequence of pHG1: A *Ralstonia eutropha* H16 encoding Key Enzymes of H2-based Lithoautotrophy and "

Y-2003) to the EMBL/GenBank/DBJ databases.

3; AAP86084.1; -.

3 AA; 20451 MW; B43832FBCC232CF4 CRC64;

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12.9%; Score 78.5; DB 2; Length 188;
arity 33.8%; Pred. No. 1.5;
onservative 8; Mismatches 30; Indels 13; Gaps 5;

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AATTMNSCI CRDDSGTDDSVDTQQQQAENSAVPTADTRSQP--RDPVRPRRRGRG 89  
| : | ||||| : || : || : || : ||  
ASD--GDS----DSGTDRSASQQSPASAQRSAPTQG-QPPARRQPAQDFPSNGFG 161

--PRRKKQNV DGL 103

1 : : : : :  
CIPFARPAALDGI 178

April 2, 2004, 10:26:03

2007



us-10-066-273-9.rai

Entry	Arch	Length	DB	ID	Description
3.1	US	460	4	US-09-252-991A-20180	Sequence 20180, A
3.0	US	287	4	US-09-252-991A-30267	Sequence 30267, A
2.8	US	1527	4	US-09-418-710-27	Sequence 27, Appl
2.8	US	1531	4	US-09-418-710-29	Sequence 29, Appl
2.3	US	433	2	US-08-466-120-2	Sequence 2, Appli
2.3	PCT	433	5	PCT-US94-07266-2	Sequence 2, Appli
2.3	US	1525	4	US-09-418-710-69	Sequence 69, Appl
2.2	US	462	2	US-08-865-597A-2	Sequence 2, Appli
2.1	US	2509	2	US-08-149-097D-35	Sequence 35, Appl
2.0	US	623	3	US-09-029-348-3	Sequence 3, Appli
2.0	US	626	3	US-09-029-348-2	Sequence 2, Appli
1.9	US	333	4	US-09-252-991A-28443	Sequence 28443, A
1.7	US	562	4	US-09-252-991A-20178	Sequence 20178, A
1.7	US	566	4	US-09-252-991A-18531	Sequence 18531, A
1.5	US	863	4	US-09-252-991A-26099	Sequence 26099, A
1.5	US	396	4	US-09-252-991A-32927	Sequence 32927, A
1.3	US	191	2	US-08-290-665A-198	Sequence 198, App
1.3	US	191	2	US-08-290-665A-199	Sequence 199, App
1.3	US	191	2	US-08-290-665A-200	Sequence 200, App
1.3	US	191	2	US-08-290-665A-201	Sequence 201, App
1.3	US	191	2	US-08-290-665A-202	Sequence 202, App
1.3	US	191	2	US-08-290-665A-203	Sequence 203, App
1.3	PCT	191	5	PCT-US95-10398-198	Sequence 198, App
1.3	PCT	191	5	PCT-US95-10398-199	Sequence 199, App
1.3	PCT	191	5	PCT-US95-10398-200	Sequence 200, App
1.3	PCT	191	5	PCT-US95-10398-201	Sequence 201, App
1.3	PCT	191	5	PCT-US95-10398-202	Sequence 202, App

ID NOS: 33142

udomonas aeruginosa  
267

larity 13.0%; Score 79; DB 4; Length 287;  
Conservative 7; Mismatches 24; Indels 4; Gaps 1;

DSVDTQQQAENS AVPTADTRSQPRDPVRPP-----RRGRGPHEPRRKQNVVG 102  
PGKRTQRRRDHPAGPVARARPGPARPRRRPGGLAGRGAGKRRRRPRQVPG 70

plication US/09418710  
482  
TION:  
ies, Michael H.  
TION: TRANSCRIPTIONAL REGULATOR  
: 06501-042001  
TION NUMBER: US/09/418,710  
DATE: 1999-10-15  
ATE: 1998-04-17  
ION NUMBER: JP 9/310027  
ION NUMBER: JP 9/116570  
ATE: 1997-04-18  
ID NOS: 73  
-SEQ for Windows Version 4.0

sapiens

larity 12.8%; Score 78; DB 4; Length 1527;  
Conservative 12; Mismatches 26; Indels 20; Gaps 3;

3TDDSVDTQQQAENS AVPTADTRSQPRDPVR-----PP-----RRGRGPHEPRR 95  
3SDEEEEEEEEEEDYEAGLRRLRPRKTIIRGKHSVIPPAARSGRRPGKPHSTRR 1314

-----QNV DGLVLD 107  
APPVDDAEVDDELVLQT 1334

lication US/09418710  
482  
TION:  
ies, Michael H.  
TION: TRANSCRIPTIONAL REGULATOR  
: 06501-042001  
TION NUMBER: US/09/418,710  
DATE: 1999-10-15  
ION NUMBER: PCT/JP98/01783  
ATE: 1998-04-17  
ION NUMBER: JP 9/310027  
ATE: 1997-10-24  
ION NUMBER: JP 9/116570  
ATE: 1997-04-18  
ID NOS: 73  
-SEQ for Windows Version 4.0

TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-418-710-29

Query Match 12.8%; Score 78; DB 4; Length 1531;  
Best Local Similarity 27.5%; Pred. No. 3.5;  
Matches 22; Conservative 12; Mismatches 26; Indels 20;

QY 48 DDSGTDSDVDTQQQAENS AVPTADTRSQPRDPVR-----PP-----RRGRGE  
Db 1259 EDDESDEEEEEEEEEEDYEAGLRRLRPRKTIIRGKHSVIPPAARSGRRPGKKE  
QY 96 KK-----QNV DGLVLD 107  
Db 1319 SQPKAPPVDDAEVDDELVLQT 1338

RESULT 5  
US-08-466-120-2  
; Sequence 2, Application US/08466120  
; Patent No. 5869284  
; GENERAL INFORMATION:  
; APPLICANT: CAO, ET AL.  
; TITLE OF INVENTION: Retinoic Acid Receptor Epsilon  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,120  
; FILING DATE: June 6, 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/07266  
; FILING DATE: 24 JUN 94  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FERRARO, GREGORY D.  
; REGISTRATION NUMBER: 36,134  
; REFERENCE/DOCKET NUMBER: 325800-354  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 433 AMINO ACIDS  
; TYPE: AMINO ACID  
; STRANDEDNESS:  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PROTEIN  
US-08-466-120-2

Query Match 12.3%; Score 75; DB 2; Length 433;  
Best Local Similarity 35.0%; Pred. No. 1.5;  
Matches 21; Conservative 12; Mismatches 23; Indels 4; (

QY 35 GAATTMGNSCICRDDSGTDDSVDTQQQAENS AVPTA-DTRSQ-PRDP--VRPPRI  
Db 29 GSQAQGGSSCILREEARMPHSAGTAGVGLAAEPTALLTRAEPSEPTEIRPPKI

RESULT 6  
PCT-US94-07266-2  
; Sequence 2, Application PC/TUS9407266

TION:  
 AO, ET AL.  
 TION: Retinoic Acid Receptor Epsilon  
 JENCES: 2  
 ADDRESS:  
 CARELLA, BYRNE, BAIN, GILFILLAN,  
 CECCHI, STEWART & OLSTEIN  
 BECKER FARM ROAD  
 AND  
 JERSEY  
 3A

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\ABLE FORM:
:      3.5 INCH DISKETTE
[BM PS/2

\STEM:  MS-DOS
WORD PERFECT 5.1
\ATION DATA:
NUMBER:  PCT/US94/07266
:  Concurrently
[ON:
TION DATA:
NUMBER:

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PERSONAL INFORMATION:  
NAME: GREGORY D.  
AGE: 36, 134  
ACCOUNT NUMBER: 325800-125  
PERSONAL INFORMATION:

SEQ ID NO: 2:  
CHARACTERISTICS:  
} AMINO ACIDS  
} ACID

LINEAR PROTEIN

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12.3%; Score 75; DB 5; Length 433;
urity 35.0%; Pred. No. 1.5;
onservative 12; Mismatches 23; Indels 4; Gaps 3;

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.MGNSCICRDDSGTDDSDVTQQQAENSAVPTA-DTRSQ-PRDP--VRPRRGRGP 90  
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ication US/09418710

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:ON:
:ns, Michael H.
:ON: TRANSCRIPTIONAL REGULATOR
06501-042001
:ION NUMBER: US/09/418,710
:ATE: 1999-10-15
:ON NUMBER: PCT/JP98/01783
:IE: 1998-04-17
:ON NUMBER: JP 9/310027
:IE: 1997-10-24
:ON NUMBER: JP 9/116570
:IE: 1997-04-18
: NOS: 73
:EQ for Windows Version 4.0

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**gapieng**

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Query Match      12.3%; Score 75; DB 4; Length 1525;
Best Local Similarity 27.9%; Pred. No. 7.9;
Matches 24; Conservative 12; Mismatches 24; Indels 26; G

QY      48 DDSGTTDSDV-----TQQQQAENSAVPTADTRSQPRDPVR-----PP-----
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QY      89 GPHEPRRKK-----QNV DGLVLD T 107
      ||| ||| :
Db      1306 KPHSTRRSQPKAPPVDAEYVDLVLQ T 1331

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RESULT 8  
 US-08-865-597A-2  
 ; Sequence 2, Application US/08865597A  
 ; Patent No. 5973131  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cao, Liang  
 ; APPLICANT: Yuen, Kwok Yung  
 ; TITLE OF INVENTION: PENNICILLUM MARNEFFEI ANTIGENIC PROTEIN 1  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036

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;
;
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/865,597A
;
; FILING DATE:
;
;

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CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Chan, Albert Wai-Kit  
REGISTRATION NUMBER: 36,479  
REFERENCE/DOCKET NUMBER: 50288-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 462 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-865-597A-2

Query Match 12.2%; Score 74.5; DB 2; Length 462;  
Best Local Similarity 29.2%; Pred. No. 1.9;  
Matches 21; Conservative 10; Mismatches 36; Indels 5; G

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QY      72  DTRSQPRDPVRP  83
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Db      383  STPAPGPAPTAP  394
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RESULT 9  
US-08-149-097D-35  
; Sequence 35, Application US/08149097D  
; Patent No. 5874236  
; GENERAL INFORMATION:  
; APPLICANT: Harpold, Michael

Ellis, Steven  
Williams, Mark  
Weldman, Daniel  
McCue, Ann  
Brenner, Robert  
ENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
ENTIONS: METHODS  
QUENCES: 40  
SE ADDRESS:  
Brown, Martin, Haller & McClain  
60 Union Street  
California  
JSA  
1-2926  
TABLE FORM:  
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IBM PC compatible  
SYSTEM: PC-DOS/MS-DOS  
PatentIn Release #1.0, Version #1.25  
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NUMBER: US/08/149,097D  
3: 05-NOV-1993  
TION: 435  
ATION DATA:  
NUMBER: 08/105,536  
3: 11-AUG-1993  
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NUMBER: WO PCT/US92/06903  
3: 14-AUG-1992  
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3: 13-JUL-1992  
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NUMBER: US 07/868,354  
3: 10-APR-1992  
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NUMBER: US 07/745,206  
3: 15-AUG-1991  
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NUMBER: US 07/620,250  
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NUMBER: US 07/482,384  
3: 20-FEB-1990  
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3: 04-APR-1989  
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3: 04-APR-1989  
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NUMBER: US 07/176,899  
3: 04-APR-1988  
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man, Stephanie L.  
IN NUMBER: 33,779  
OCKET NUMBER: 6362-55038  
TION INFORMATION:  
(619) 238-0999  
(619) 238-0062  
SEQ ID NO: 35:  
ACTERISTICS:  
09 amino acids  
to acid  
S: single  
linear  
protein  
NO  
NO  
internal  
CE:

OTHER INFORMATION: /product= "AlphaA-1 subunit of  
OTHER INFORMATION: human calcium channel"  
US-08-149-097D-35  
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Best Local Similarity 24.2%; Pred. No. 23;  
Matches 31; Conservative 9; Mismatches 39; Indels 49;  
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Db 2251 SRSPSEG-----REHMAHRQSSSVSGSPAPSTSGTSTPRRGRRLPQPESTPRP  
QY 45 -ICRDDSGETDSDVDTQQQAENSAV-----PTADTRSQPRDPVR  
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QY 88 RGPHEPRR 95  
Db 2366 RSPRMERR 2373  
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US-09-029-348-3  
; Sequence 3, Application US/09029348  
; Patent No. 6171827  
; GENERAL INFORMATION:  
; APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER  
; TITLE OF INVENTION: NOVEL PROCOLLAGENS  
; FILE REFERENCE: G087857PUS LISTING  
; CURRENT APPLICATION NUMBER: US/09/029,348  
; CURRENT FILING DATE: 1998-05-07  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 623  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: SEQUENCE  
; OTHER INFORMATION: DERIVED FROM cDNA OF PROCOLLAGENS  
US-09-029-348-3  
Query Match 12.0%; Score 73; DB 3; Length 623;  
Best Local Similarity 28.8%; Pred. No. 4.2;  
Matches 30; Conservative 10; Mismatches 36; Indels 28;  
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QY 56 V-DTQQQAENSAVP---TADTRSQPRDPVRPPRRGRGPHEPR 94  
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US-09-029-348-2  
; Sequence 2, Application US/09029348  
; Patent No. 6171827  
; GENERAL INFORMATION:  
; APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER  
; TITLE OF INVENTION: NOVEL PROCOLLAGENS  
; FILE REFERENCE: G087857PUS LISTING  
; CURRENT APPLICATION NUMBER: US/09/029,348  
; CURRENT FILING DATE: 1998-05-07  
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; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: SEQUENCE



ON: DERIVED FROM CDNA OF PROCOLLAGENS

12.0%; Score 73; DB 3; Length 626;  
urity 28.8%; Pred. No. 4.2;  
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3 application US/09252991A

ON: J. Rubenfield et al.  
ON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
ON: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

107196.136  
ION NUMBER: US/09/252,991A  
DATE: 1999-02-18  
N NUMBER: US 60/074,788  
E: 1998-02-18  
N NUMBER: US 60/094,190  
E: 1998-07-27  
NOS: 33142

lomonas aeruginosa

11.9%; Score 72.5; DB 4; Length 333;  
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8 application US/09252991A

ON: J. Rubenfield et al.  
ON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
ON: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

107196.136  
ION NUMBER: US/09/252,991A  
DATE: 1999-02-18  
N NUMBER: US 60/074,788  
E: 1998-02-18  
N NUMBER: US 60/094,190  
E: 1998-07-27  
NOS: 33142

lomonas aeruginosa

Query Match 11.7%; Score 71.5; DB 4; Length 562;  
Best Local Similarity 29.7%; Pred. No. 5.5;  
Matches 22; Conservative 6; Mismatches 29; Indels 17; G

QY 36 AATTMGNSCICRDSGTDSDVTQQAENS AVPTADTRS QPRDPV RPRRGRGP 17  
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QY 94 ----RRKKQNV DGL 103  
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RESULT 14  
US-09-252-991A-18531  
; Sequence 18531, Application US/09252991A  
; Patent No. 6551795

GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 18531  
; LENGTH: 566  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-18531

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Matches 29; Conservative 10; Mismatches 37; Indels 47; G

QY 23 LEEHIAHFLGTGGAATTMGNSC--ICRDSGTDSDVD-----TQQAENSA  
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QY 72 DTRS QPRDP-----VRPPRR-----GRGPH  
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QY 96 KKQ 98  
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Db 238 RQR 240

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; Sequence 26099, Application US/09252991A  
; Patent No. 6551795

GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
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US-09-252-991A-26099

**us-10-066-273-9.rai**

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11.7%; Score 71; DB 4; Length 863;
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April 2, 2004, 10:27:12

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

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sting first 45 summaries

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SUMMARIES

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.0	117	14	US-10-002-796-9		Sequence 9, Appli
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.0	117	14	US-10-066-494-9		Sequence 9, Appli
.0	117	14	US-10-066-269-9		Sequence 9, Appli
.0	117	14	US-10-006-856A-6		Sequence 6, Appli
.0	117	14	US-10-066-211-9		Sequence 9, Appli
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35	609	100.0	117	14	US-10-223-083-6	Sequence
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ALIGNMENTS

RESULT 1

US-09-946-374-6  
; Sequence 6, Application US/09946374  
; Publication No. US20030073129A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nuc.  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C1  
; CURRENT APPLICATION NUMBER: US/09/946,374  
; CURRENT FILING DATE: 2001-09-04  
; PRIOR APPLICATION NUMBER: 60/098716  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098723  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098749  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098750

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TE: 1998-09-02  
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ON NUMBER: 60/098843  
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ION:

J. Ashkenazi

in P. Baker

id A. Botstein

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oleone Ferrara

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nie P. Mather

y A. Napier

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ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

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P3130RIC7

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; APPLICANT: Avi J. Ashkenazi  
; APPLICANT: Kevin P. Baker  
; APPLICANT: David A. Botstein  
; APPLICANT: Luc Desnoyers  
; APPLICANT: Dan L. Eaton  
; APPLICANT: Napoleone Ferrara  
; APPLICANT: Sherman Fong  
; APPLICANT: Wei-Qiang Gao  
; APPLICANT: Hanspeter Gerber  
; APPLICANT: Mary E. Gerritsen  
; APPLICANT: Audrey Goddard  
; APPLICANT: Paul J. Godowski  
; APPLICANT: Austin L. Gurney  
; APPLICANT: Ivar J. Kljavin  
; APPLICANT: Jennie P. Mather  
; APPLICANT: Mary A. Napier  
; APPLICANT: James Pan  
; APPLICANT: Nicholas F. Paoni  
; APPLICANT: Margaret Ann Roy  
; APPLICANT: Timothy A. Stewart  
; APPLICANT: Daniel Tumas  
; APPLICANT: Colin K. Watanabe  
; APPLICANT: P. Mickey Williams  
; APPLICANT: William I. Wood  
; APPLICANT: Zemin Zang  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC  
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ION:

J. Ashkenazi  
in P. Baker  
id A. Botstein  
Desnoyers  
L. Eaton  
oleone Ferrara  
rman Fong  
-Qiang Gao  
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rey Goddard  
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thy A. Stewart  
iel Tumas  
in K. Watanabe  
ickey Williams  
liam I. Wood  
in Zang

ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
ION: ACIDS ENCODING THE SAME

P3130R1C2

ION NUMBER: US/10/066,273

DATE: 2002-02-01

ION NUMBER: 10/002,796

FE: 2001-11-15

ION NUMBER: 60/056974

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ION NUMBER: 60/059115

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FE: 1997-11-21

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ION NUMBER: 60/069694

FE: 1997-12-16

ION NUMBER: 60/074086

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FE: 1998-02-09

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FE: 1998-03-25

ION NUMBER: 60/081049

FE: 1998-04-08

ION NUMBER: 60/095998

FE: 1998-08-10

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ION NUMBER: PCT/US99/21547

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; Sequence 9, Application US/10066494  
; Publication No. US20030032063A1  
; GENERAL INFORMATION:  
; APPLICANT: Avi J. Ashkenazi  
; APPLICANT: Kevin P. Baker  
; APPLICANT: David A. Botstein  
; APPLICANT: Luc Desnoyers  
; APPLICANT: Dan L. Eaton  
; APPLICANT: Napoleone Ferrara  
; APPLICANT: Sherman Fong  
; APPLICANT: Wei-Qiang Gao  
; APPLICANT: Hanspeter Gerber  
; APPLICANT: Mary E. Gerritsen  
; APPLICANT: Audrey Goddard  
; APPLICANT: Paul J. Godowski  
; APPLICANT: Austin L. Gurney  
; APPLICANT: Ivar J. Kljavin  
; APPLICANT: Jennie P. Mather  
; APPLICANT: Mary A. Napier  
; APPLICANT: James Pan  
; APPLICANT: Nicholas F. Paoni  
; APPLICANT: Margaret Ann Roy  
; APPLICANT: Timothy A. Stewart  
; APPLICANT: Daniel Tumas  
; APPLICANT: Colin K. Watanabe  
; APPLICANT: P. Mickey Williams  
; APPLICANT: William I. Wood  
; APPLICANT: Zemin Zang  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NU  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3130R1C9  
; CURRENT APPLICATION NUMBER: US/10/066,494  
; CURRENT FILING DATE: 2002-02-01  
; PRIOR APPLICATION NUMBER: 10/002,796  
; PRIOR FILING DATE: 2001-11-15  
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RESULT 7  
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; Publication No. US20030040014A1

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J. Ashkenazi  
vin P. Baker  
vid A. Botstein  
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a L. Eaton  
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i-Qiang Gao  
aspeter Gerber  
ry E. Gerritsen  
frey Goddard  
il J. Godowski  
stin L. Gurney  
ar J. Kljavin  
mie P. Mather  
cy A. Napier  
nes Pan  
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iel Tumas  
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ickey Williams  
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ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
ION: ACIDS ENCODING THE SAME  
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100.0%; Score 609; DB 14; Length 117;  
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r, Kevin P.  
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APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
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APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nuc  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2830P1C14  
CURRENT APPLICATION NUMBER: US/10/006,856A  
NUMBER OF SEQ ID NOS: 477  
Prior Application removed - See File Wrapper or Palm  
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FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 1-16  
OTHER INFORMATION: Signal Peptide  
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LOCATION: 18-24, 32-38, 34-40, 35-41, 51-57  
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NAME/KEY: misc feature  
LOCATION: 22-26, 50-54, 113-117  
OTHER INFORMATION: Casein Kinase II Phosphorylation Site.  
US-10-006-856A-6

Query Match 100.0%; Score 609; DB 14; Length 117;  
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RESULT 9  
US-10-066-211-9  
Sequence 9, Application US/10066211  
Publication No. US2003004484A1  
GENERAL INFORMATION:

APPLICANT: Avi J. Ashkenazi  
APPLICANT: Kevin P. Baker  
APPLICANT: David A. Botstein  
APPLICANT: Luc Desnoyers  
APPLICANT: Dan L. Eaton  
APPLICANT: Napoleone Ferrara  
APPLICANT: Sherman Fong  
APPLICANT: Wei-Qiang Gao  
APPLICANT: Hanspeter Gerber  
APPLICANT: Mary E. Gerritsen  
APPLICANT: Audrey Goddard  
APPLICANT: Paul J. Godowski  
APPLICANT: Austin L. Gurney  
APPLICANT: Ivar J. Kljavin  
APPLICANT: Jennie P. Mather  
APPLICANT: Mary A. Napier  
APPLICANT: James Pan  
APPLICANT: Nicholas F. Paoni

Garet Ann Roy  
nothy A. Stewart  
liel Tumas  
lin K. Watanabe  
Mickey Williams  
lliam I. Wood  
nin Zang  
TION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
TION: ACIDS ENCODING THE SAME  
: P3130R1C8  
TION NUMBER: US/10/066,211  
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ON NUMBER: 60/145698

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; PRIOR FILING DATE: 2001-05-25

ON NUMBER: 09/870574  
FE: 2001-05-30  
ON NUMBER: 09/872035  
FE: 2001-06-01  
ON NUMBER: 09/886342  
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ON NUMBER: PCT/US98/14552  
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ON NUMBER: PCT/US99/20111  
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ON NUMBER: PCT/US99/21090  
FE: 1999-09-15  
ON NUMBER: PCT/US99/21547

100.0%; Score 609; DB 14; Length 117;  
arity 100.0%; Pred. No. 1.7e-58;  
onservative 0; Mismatches 0; Indels 0; Gaps 0;

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ication US/10066193  
JS20030044902A1  
CON:  
J. Ashkenazi  
in P. Baker  
id A. Botstein  
Desnoyers  
L. Eaton  
pleone Ferrara  
aman Fong  
-Qiang Gao  
peter Gerber  
/ E. Gerltsen  
ey Goddard  
l J. Godowski  
in L. Gurney  
c J. Kljavin  
ie P. Mather  
/ A. Napier  
as Pan  
olas F. Paoni  
aret Ann Roy  
thy A. Stewart  
iel Tumas

APPLICANT: Colin K. Watanabe  
APPLICANT: P. Mickey Williams  
APPLICANT: William I. Wood  
APPLICANT: Zemin Zang  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC  
TITLE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3130R1C3  
CURRENT APPLICATION NUMBER: US/10/066,193  
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; PRIOR FILING DATE: 2001-06-01  
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; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 100.0%; Score 609; DB 14; Length 117;  
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RESULT 11  
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; Publication No. US20030054406A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nuc  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C4  
; CURRENT APPLICATION NUMBER: US/10/006,818A  
; CURRENT FILING DATE: 2001-12-06  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 6  
; LENGTH: 117  
; TYPE: PRT



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feature  
32-38, 34-40, 35-41, 51-57  
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feature  
50-54, 113-117  
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ication US/10015393A  
JS20030069179A1  
ION:  
Kevin P.  
stein, David  
oyers, Luc  
n, Dan I.  
ara, Napoleone  
f, Sherman  
Wei-Qiang  
ard, Audrey  
owski, Paul J.  
naldi, Christopher J.  
ey, Austin L.  
lan, Kenneth J.  
James  
ai, Nicholas F.  
ION: Secreted and Transmembrane Polypeptides and Nucleic  
ION: Acids Encoding the Same  
P2830P1C46  
ION NUMBER: US/10/015,393A  
DATE: 2002-06-10  
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feature  
6, 50-54, 113-117  
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100.0%; Score 609; DB 14; Length 117;

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RESULT 13  
US-10-015-869A-6  
Sequence 6, Application US/10015869A  
Publication No. US20030073130A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan I.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nuc  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2830P1C45  
CURRENT APPLICATION NUMBER: US/10/015,869A  
CURRENT FILING DATE: 2002-06-25  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 477  
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LENGTH: 117  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 1-16  
OTHER INFORMATION: Signal Peptide  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 18-24, 32-38, 34-40, 35-41, 51-57  
OTHER INFORMATION: N-Myristoylation Site.  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 22-26, 50-54, 113-117  
OTHER INFORMATION: Casein Kinase II Phosphorylation Site.  
US-10-015-869A-6  
Query Match 100.0%; Score 609; DB 14; Length 117;  
Best Local Similarity 100.0%; Pred. No. 1.7e-58;  
Matches 117; Conservative 0; Mismatches 0; Indels 0; G  
QY 1 MIVFGWAVFLASRLSGQLLTLEEHIAHFLGTGGAAATMGNSCICRDDSGTDDSV  
Db 1 MIVFGWAVFLASRLSGQLLTLEEHIAHFLGTGGAAATMGNSCICRDDSGTDDSV  
QY 61 QOAENSAVPTADTRSQPRDPVPPRRGRGPHPRKKQNVGDLVLDTLAVIRTLVD  
Db 61 QOAENSAVPTADTRSQPRDPVPPRRGRGPHPRKKQNVGDLVLDTLAVIRTLVD  
RESULT 14  
US-10-012-121A-6  
Sequence 6, Application US/10012121A  
Publication No. US20030073810A1

TION:
er, Kevin P.
stein, David
noyers, Luc
on, Dan I.
rara, Napoleone
g, Sherman
, Wei-Qiang
dard, Audrey
owski, Paul J.
imaldi, Christopher J.
ney, Austin L.
ilan, Kenneth J.
a, James
ni, Nicholas F.
TION: Secreted and Transmembrane Polypeptides and Nucleic
TION: Acids Encoding the Same
: P2830P1C20
TION NUMBER: US/10/012,121A
DATE: 2001-12-07
ion removed - See File Wrapper or Palm
ID NOS: 477

o sapiens
peptide
6
TION: Signal Peptide
c feature
24, 32-38, 34-40, 35-41, 51-57
TION: N-Myristoylation Site.

c feature
26, 50-54, 113-117
TION: Casein Kinase II Phosphorylation Site.

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noyers, Luc
on, Dan I.
rara, Napoleone
ng, Sherman
o, Wei-Qiang
ddard, Audrey
dowski, Paul J.
imaldi, Christopher J.
rney, Austin L.
ilan, Kenneth J.
n, James
ni, Nicholas F.
TION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same
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Query Match 100.0%; Score 609; DB 14; Length 117;  
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Search completed: April 2, 2004, 10:28:05  
Job time : 41 secs